

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 19, 2005, 15:23:30 : Search time 199 Seconds
(without alignments)
2021.040 Million cell updates/sec

Title: US-10-799-676-2
Perfect score: 3742
Sequence: 1 MSSRKVLAIQARKRPKEK.....MVPEKASAGECLRHPLWLS 699

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt.02.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3626	96.9	688	Q81YQ3	Q81YQ3 homo sapien
2	3622	96.8	675	O75220	O75220 homo sapien
3	3613	96.6	688	Q6NUL0	Q6NUL0 homo sapien
4	3613	96.6	688	AaH68547	AaH68547 homo sapi
5	3586	95.8	686	P78362	P78362 homo sapien
6	3574	95.5	675	O75221	O75221 homo sapien
7	3395.5	90.7	681	O54781	O54781 mus musculu
8	3392	90.6	682	Q8VCD9	Q8VCD9 mus musculu
9	2810	75.1	546	Q6VIX2	Q6VIX2 homo sapien
10	2810	75.1	546	AAQ63886	AAQ63886 homo sapi
11	2070.5	55.3	655	Q12890	Q12890 homo sapien
12	2061.5	55.1	826	Q96SB4	Q96SB4 homo sapien
13	2061	55.1	634	Q6PGU8	Q6PGU8 brachydanio
14	2061	55.1	634	AaH56825	AaH56825 brachydian
15	2059.5	55.0	655	Q81Y12	Q81Y12 homo sapien
16	2058	55.0	648	Q99JT3	Q99JT3 mus musculu
17	2053	54.9	648	O70193	O70193 mus musculu
18	2047.5	54.7	646	Q8VHL3	Q8VHL3 cricetus
19	2037	54.4	648	O70551	O70551 mus musculu
20	1950	52.1	605	Q6INS4	Q6INS4 xenopus lae
21	1950	52.1	605	AAH72199	AAH72199 xenopus l
22	1904	50.9	565	1 ST23_MOUSE	Q920g2 mus musculu
23	1882	50.3	533	1 ST23_HUMAN	Q9UPE1 homo sapien
24	1873	50.1	563	Q6V9W0	Q6V9W0 rattus norv
25	1873	50.1	563	2 AAQ55283	AAQ55283 rattus no
26	1525	40.8	764	Q8ML99	Q8ML99 drosophila
27	1524	40.7	764	Q9GSP5	Q9GSP5 drosophila
28	1476	39.4	306	2 O08551	O08551 mus musculu
29	1377.5	36.8	607	2 O8ML98	O8ML98 drosophila
30	1374	36.7	698	2 Q9XVY0	Q9XVY0 caenorhabdi
31	1374	36.7	1093	1 YKD5_CABEL	Q03563 caenorhabdi

32	1361.5	36.4	774	2	Q9XVX9	Q9XVX9 caenorhabdi
33	1361.5	36.4	774	2	CAA79542	CAA79542 caenorhab
34	1260	33.7	612	2	Q7Q7G5	Q7Q7G5 anopheles 9
35	1245	33.3	749	2	Q8T3S1	Q8T3S1 drosophila
36	1216	32.5	816	2	Q9VNV0	Q9VNV0 drosophila
37	1170	31.3	221	2	Q8CBI1	Q8CBI1 mus musculu
38	1075	28.7	538	2	Q8LGG5	Q8LGG5 arabidopsis
39	1068	28.5	538	2	Q9FE52	Q9FE52 arabidopsis
40	1066.5	28.5	534	2	Q9FYC5	Q9FYC5 arabidopsis
41	1065.5	28.5	513	2	Q870S3	Q870S3 neurospora
42	1065.5	28.5	578	2	Q7S3A6	Q7S3A6 neurospora
43	1043.5	27.9	556	2	Q8W306	Q8W306 oryza sativ
44	1039	27.8	529	2	Q9FYB3	Q9FYB3 arabidopsis
45	1026	27.4	529	2	Q94AX8	Q94AX8 arabidopsis

ALIGNMENTS

RESULT 1
Q81YQ3
ID Q81YQ3 PRELIMINARY; PRT; 688 AA.
AC Q81YQ3;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE SFRS protein kinase 2, isoform b.
GN Name=SRPK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC035214; AaH35214.1; -.
DR HSP; Q03656; IHW.
DR Genew; HGNC:11306; SRPK2.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot-Kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.

	677	MLEWPEKRAAGECLRHFWLNS	699	
Oy	.			
Dbl	686	MLEWVPEKRAGACGLRHPWLNS	688	
RESULT 5	PRES32	PRELIMINARY;	PRT; 686 AA.	
ID	F78362			
AT	P78362;			
DC	01-MAY-1997 (TrEMBLrel. 03, Created)			
DT	01-MAY-1997 (TrEMBLrel. 03, Last sequence update)			
DI	01-MAR-2004 (TrEMBRel. 26, Last annotation update)			
DE	Serine kinase SRPK2			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
NCBI TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	[1]_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=98139536; PubMed=9472028;			
RA	Wang H.Y., Lin W., Dyck J.A., Yeakley J.M., Songyang Z., Cantley L.C., Fu X.D.;			
RT	"SRPK2: a differentially expressed SR protein-specific kinase involved			
RD	in mediating the interaction and localization of pre-mRNA splicing			
RE	factors in mammalian cells.";			
J. Cell Biol.	140:737-750(1998).			
-!-	SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
ESBUI; Q88666; AAC05299.1; --				
CRC64;				
GO:	GO:0005634; C:nucleus; TAS.			
GO:	GO:0004672; P:protein kinase activity; TAS.			
GO:	GO:0008380; P:rna_splicing; TAS.			
GO:	GO:000245; P:spliceosome assembly; TAS.			
IPIPR011009; Kinase like.				
IPIRO00719; Prot_kinase.				
IPIRO08271; Ser_thr_pkin_AS.				
PFam; PF00069; Pkinase; 1.				
ProDom; PD000001; Prot_kinase; 2.				
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.				
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.				
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.				
KQ	ATP-binding; kinase, Serine/threonine-protein kinase; Transferase.			
SW	SEQUENCE 686 AA; 77423 MW; 189F16E9FEFBAS82 CRC64;			
Query Match	95.8%; Score 3586; DB 2; Length 686;			
Best Local Similarity	98.2%; Pred.No. 7.9e-149;			
Matches 67l; Conservative	4; Mismatches 6; Indels 2; Gaps 2;			
OY	17 KKEHIPKPPOOKAPLVPPPPPPPPLDPPTTTPPEEEIIGSDDEEDPADYCK 76	:	:	
Dbl	: : :	:	:	
	6 EKSSSERPEOQAALPVPPPPPPPPLDPTTTPPEEEIIGSDDEEQADPYCK 65	:	:	
OY	77 GGYPHVKIGDLFNGRHYHVIRKLWGHSFTVMWCMDMQGKFVAMKVKKSAHQYTETALDE 136	:	:	
Dbl	GGYPHVKIGDLFNGRHYHVIRKLWGHSFTVMWCMDMQGKFVAMKVKKSAHQYTETALDE 125	:	:	
OY	137 IKLLKCVRSDSPDNKMVOLIDDFKISGMNGIHVCMVFLGHLLKWIKSNVOGI 196	:	:	
Dbl	IKLLKCVRSDSPDNKMVOLIDDFKISGMNGIHVCMVFLGHLLKWIKSNVOGI 185	:	:	
OY	197 PVRCVKSIIROYLGVDYLHSKCKLIHTDDIPENILMCVVDAVYRRMAAEATEWKAGAP 256	:	:	
Dbl	PVRCVKSIIROYLGVDYLHSKCKLIHTDDIPENILMCVVDAVYRRMAAE-PEWQKAGAP 244	:	:	
OY	257 PPSSGSAVTAPOQGPGTKISKNNKKLKXKOQLERLOSLIEELEREARKIIKEN 316	:	:	
Dbl	PPSSGSAVTAPOQPDKIGKIKNKKKKKKRKORQAEELLERLOSLIEELEREARKIIKEN 304	:	:	
OY	317 ITSGAASNODGEYCPEVKLTWTGLEAAEAETAKDNGEAADOEKEDAENIKEDED 376	:	:	
Dbl	ITGAASPNDGDCEYCPEVKLTWTGLEAAEAETAKDNGEAADOEKEDAENIKEDED 364	:	:	
OY	377 VDDELANIDPTTESPKTNIGHIFPSLEQQLEDDEDDECPCNPSEYNDFPNAESDY 436	:	:	

		VQSLANIDPTWIESPKTNHIEGPFSLBEOQLDDDEDCPPEEYNLPDPAESDY	424
365	Db		
		TYSSTSYEQFNGELPNGRHKIPESOPPEESTLSFGSLEPVCACSVLSEGSPLTEQBESSP	496
437	Qy		
		TYSSTSYEQFNGELPNGRHKIPESOPPEESTLSFGSLEPVCACSVLSEGSPLTEQBESSP	484
425	Db		
		SHDRSRVTSASSTGDLPKAKTRAADLLNPLDPNRNADKIRVKIADLGNACWVHKFTEDI	556
497	Qy		
		SHDRSRVTSASSTGDLPKAKTRAADLLNPLDPNRNDKIRVKIADLGNACWVHKFTEDI	544
485	Db		
		QTROYRSIEVLIGAGYSTPADIWSTACAFELATGDYLFEPHSGSDYSEDDEHIAHI TEL	616
557	Qy		
		QTROYRSIEVLIGAGYSTPADIWSTACAFELATGDYLFEPHSGSDYSEDDEHIAHI TEL	604
545	Db		
		LGSISPRIFALSGCKYSREFFNRRRGELRHITKLKPWSLFDVLVEKYGWPHEDAAQAQTFDFLI P	676
617	Qy		
		LGSISPRIFALSGCKYSREFFNRRRGELRHITKLKPWSLFDVLVEKYGWPHEDAAQAQTFDFLI P	664
605	Db		
		MLEMVPKRASAGECLRHPWLNS	699
677	Qy		
		MLEMVPKRASAGEC-RHPWLNS	686
665	Db		

RESULT 6

O75221 PRELIMINARY; PRT; 675 AA.

ID O75221

AC 075221; (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE WUGSC:H RG152G17.1b protein (Fragment).

GN Name=WUGSC:H RG152G17.1b;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RN RN

RN RN

RN RN

RA Rohlffing T., O'Neal D.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RN RN

RN RN

RA SEQUENCE FROM N.A.

RA Waterston R.H.;

RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RN RN

RN RN

RN RN

RA SEQUENCE FROM N.A.

RA Waterston R.;

RA Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

RN [4]

RN RN

RN RN

RA SEQUENCE FROM N.A.

RA Waterston R.;

RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; AC005070; AAC29141.1; -.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR008271; Prot kinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 2.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

FT NON_TER 1

FT NON_TER 1

SEQ SEQUENCE 675 AA; 76102 MW; BOFF1532AE129CEB CRC64;

Query Match 95.5%; Score 3574; DB 2; Length 675;

Best Local Similarity 98.5%; Pred.No. 2.6e-148;

	Matches	665;	Conservative	5;	Mismatches	5;	Indels	0;	Gaps
Qy	25	PEPOQKAPLVP	PPPPPPPPPPPPPPPPPPPP	PPDP	PPPEE	EEILGSDDE	BEQDDPADYCKGGYHPVKI	84	
Db	1	PEPOQKAPLVP	PPPPPPPPPPPPPPPPPPPP	PPDP	PPPEE	EEILGSDDE	BEQDDPADYCKGGYHPVKI	60	
Qy	85	GDLPNGRYHVI	RKLGWGHFSTVWLCWDMQGR	FRVAMKVVVKS	AQHVTETALDEIKL	LKCVR		144	
Db	61	GDLPNGRYHVI	RKLGWGHFSTVWLCWDMQGR	FRVAMKVVVKS	AQHVTETALDEIKL	LKCVR		120	
Qy	145	ESDPSD	DNKMVVLIDDFKISGWN	GHVCMVFEVLGHHLKWI	IKSNYQGLPVRCV	KSI		204	
Db	121	ESDPSD	DNKMVVLIDDFKISGWN	GHVCMVFEVLGHHLKWI	IKSNYQGLPVRCV	KSI		180	
Qy	205	IRQVLQGLDYL	HSCKIIHTDIKPENILMCV	DDDAYVRMAAE	ATEWQKAGAPPP	SGS		264	
Db	181	IRQVLQGLDYL	HSCKIIHTDIKPENILMCV	DDDAYVRMAAE	ATEWQKAGAPPP	SGS		240	
Qy	265	TAPOOKDIGI	SKNKKKLKKQKRQABLL	KKRLOEIEELBREAR	KIIEENITSA	SPSN		324	
Db	241	TAPOOKDIGI	SKNKKKLKKQKRQABLL	KKRLOEIEELBREAR	KIIEENITSA	SPSN		300	
Qy	325	DQGEYCPEVK	LKTTGLEEAAEATKONGE	AEQOEKE	DAEKENI	EKDEDDVDOELANI		384	
Db	301	DQGEYCPEVK	LKTTGLEEAAEATKONGE	AEQOEKE	DAEKENI	EKDEDDVDOELANI		360	
Qy	385	DPTWIESPK	NGHTE	NGPFSLE	QQLDDEDD	DEDCPNEE	YNLDEPNAESDY	444	
Db	361	DPTWIESPK	NGHTE	NGPFSLE	QQLDDEDD	DEDCPNEE	YNLDEPNAESDY	420	
Qy	445	FNGELPNGR	HKIPESQ	PFSTSLF	SGSLEPV	ACGSLSE	GSPLTEQESSPSH	504	
Db	421	FNGELPNGR	HKIPESQ	PFSTSLF	SGSLEPV	ACGSLSE	GSPLTEQESSPSH	480	
Qy	505	SASSTGDL	PKAKTFAADLLVNPDL	PRNADKIR	VKIADIGN	ACVWHKHFTED	QTRQYRSI	564	
Db	481	SASSTGDL	PKAKTFAADLLVNPDL	PRNADKIR	VKIADIGN	ACVWHKHFTED	QTRQYRSI	540	
Qy	565	EVILIGAGY	STPADT	WSTACMA	FELATGDY	LPFEPH	SGEDYSRDE	624	
Db	541	EVILIGAGY	STPADT	WSTACMA	FELATGDY	LPFEPH	SGEDYSRDE	600	
Qy	625	ALSGKYSR	EFNRRG	ELRHITK	LKPWSLFD	VLVEKYG	WPHEDAAQ	684	
Db	601	AMLGKYSK	EFRTKRG	ELRHITK	LKPWSLFD	VLVEKYG	WPHEDAAQ	660	
Qy	685	RASAGECL	RHPWLS	699					
Db	661	RASAGECL	RHPWLS	675					
RESULT 7									
O54781									
ID	O54781		PRELIMINARY;		PRT;		681	AA.	
AC	O54781;								
DT	01-JUN-1998	(TrEMBLrel. 06, Created)							
DT	01-JUN-1998	(TrEMBLrel. 06, Last sequence update)							
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)							
DE	SRPK2.								
GN	Name=SRpk2;								
OS	Mus musculus								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
OX	NCBI_TaxID=10090;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Kuroyanagi N., Onogi H., Wakabayashi T., Gagiwara M.;								
RT	"Novel SR-protein-specific kinase, SRPK2, disassembles nuclear								
RT	speckles.";								
RL	Blotchen. Biophys. Res. Commun. 0:0-0(1998).								
CC	-/- SIMILARITY: Belongs to the Ser/Thr protein kinase family.								
DR	EMBL; AB006036; BAA24055.1; -.								
DR	PIR; JCS929; JCS929.								


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Db 124 IKLLKCVRESDDPSDPNKMVQVLDIDFKISGMNGIHVCMVFEVLGHLLKWIISNYQGL 183
Qy 197 PVRCKVSIIRVQLGDLVHSCCKIIHTDIKPNILMVCVDDAYVRRMAAEATEWQKAGAP 256
Db 184 PVRCKVSIIRVQLGDLVHSCCKIIHTDIKPNILMVCVDDAYVRRMAAEATEWQKAGAP 243
Qy 257 PPSGSAVSTAPQPKPGIKSKNKKLKKQKQKQAELEKRLQEIIEELREAEKRIIEN 316
Db 244 PPSGSAVSTAPQPKPGIKSKNKKLKKQKQKQAELEKRLQEIIEELREAEKRIIEN 303
Qy 317 ITSAAPSND - QDGEYCPEVKLTGTELEAAEATKDNGEAEDEQEKEDAENIEKORD 375
Db 304 ITSAEASGQDGEYCPEVTLKAADLEDTEETAKDNGEVEDQEKEDAENAEKORD 363
Qy 376 DVDQELANIDPTWIESPKTNHENGPFSLBOOLDDEDDPCPNPEYNLDEPNVARD 435
Db 364 DVDQELANIDPTWIESPKTNHENGPFSLBOOLDDEDDPCPNPEYNLDEPNVARD 423
Qy 436 YTYSSSYEQFNGELPNGRHKIPESQPFESTSLFSGSLPVCAGSVLSEGSPLTQESS 495
Db 424 YTYSSSYEQFNGELPNQHKT-----SERPTPLFSGPLPVCAGSVLSEGSPLTQESS 478
Qy 496 PSHDRSRTVSASSTGDLPAKTRAADLLVNPDPNADKIRVKIADLGNACVWHKHFTED 555
Db 479 PSHDRSRTVSASSTGDLPAKTRAADLLVNPDPNADKIRVKIADLGNACVWHKHFTED 538
Qy 556 IOTRQVRSIEVLIGAGYSTPADISTACMAFELATGDLFYPHSGSDYSRDEHIAHIE 615
Db 539 IOTRQVRSIEVLIGAGYSTPADISTACMAFELATGDLFYPHSGSDYSRDEHIAHIE 598
Qy 616 LGSGIPRHFAKSKYSREFFNRRGELRHITKLPKNSLFDVLVEKYGWPHEDAQAFTDFLI 675
Db 599 LGSGIPRHFAKSKYSREFFNRRGELRHITKLPKNSLFDVLVEKYGWPHEDAQAFTDFLI 658
Qy 676 PMLWVPEKRSAGELRHPWLNS 699
Db 659 PMLWVPEKRSAGELRHPWLNS 682
RESULT 9
Q6V1X2 PRELIMINARY; PRT; 546 AA.
AC Q6V1X2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE SFRS protein kinase 2 isoform c.
GN Name=SRPK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sha J.H., Zhou Z.M., Li J.M.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AY354201; AAQ63886.1; -.
DR GO; GO:0016301; F_kinase activity; IEA.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; I.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
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SQ SEQUENCE 546 AA; 61049 MW; 5F1DB6805A6CD79C CRC64;
Query Match 75.1%; Score 2810; DB 2; Length 546;
Best Local Similarity 98.3%; Pred. No. 4.6e-115;
Matches 525; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 17 KREKHPKPEPOOKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 76
Db 6 EKSSSERPEPOOKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 65
Qy 77 GGYHPVKIGDLFNGRHYHVRKLGWGHFSTWLCWDMQGRFVAMKVVKSAQHYTETALDE 136
Db 66 GGYHPVKIGDLFNGRHYHVRKLGWGHFSTWLCWDMQGRFVAMKVVKSAQHYTETALDE 125
Qy 137 IKLLKCVRESDDPSDPNKMVQVLDIDFKISGMNGIHVCMVFEVLGHLLKWIISNYQGL 196
Db 126 IKLLKCVRESDDPSDPNKMVQVLDIDFKISGMNGIHVCMVFEVLGHLLKWIISNYQGL 185
Qy 197 PVRCKVSIIRVQLGDLVHSCCKIIHTDIKPNILMVCVDDAYVRRMAAEATEWQKAGAP 256
Db 186 PVRCKVSIIRVQLGDLVHSCCKIIHTDIKPNILMVCVDDAYVRRMAAEATEWQKAGAP 245
Qy 257 PPSGSAVSTAPQPKPGIKSKNKKLKKQKQKQAELEKRLQEIIEELREAEKRIIEN 316
Db 246 PPSGSAVSTAPQPKPGIKSKNKKLKKQKQKQAELEKRLQEIIEELREAEKRIIEN 305
Qy 317 ITSAAPSNDQDGEYCPEVKLTGTELEAAEATKDNGEAEDEQEKEDAENIEKDEDD 376
Db 306 ITSAAPSNDQDGEYCPEVKLTGTELEAAEATKDNGEAEDEQEKEDAENIEKDEDD 365
Qy 377 DVDQELANIDPTWIESPKTNHENGPFSLBOOLDDEDDPCPNPEYNLDEPNVARD 436
Db 366 DVDQELANIDPTWIESPKTNHENGPFSLBOOLDDEDDPCPNPEYNLDEPNVARD 425
Qy 437 YTYSSSYEQFNGELPNGRHKIPESQPFESTSLFSGSLPVCAGSVLSEGSPLTQESS 496
Db 426 YTYSSSYEQFNGELPNGRHKIPESQPFESTSLFSGSLPVCAGSVLSEGSPLTQESS 485
Qy 497 SHDRSRTVSASSTGDLPAKTRAADLLVNPDPNADKIRVKIADLGNACVWHK 550
Db 486 SHDRSRTVSASSTGDLPAKTRAADLLVNPDPNADKIRVKIADLGNACVWHK 539
RESULT 10
AAQ63886 PRELIMINARY; PRT; 546 AA.
AC AAQ63886;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE SFRS protein kinase 2 isoform c.
GN SRPK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Sha J.H., Zhou Z.M., Li J.M.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY354201; AAQ63886.1; -.
KW Kinase.
SQ SEQUENCE 546 AA; 61049 MW; 5F1DB6805A6CD79C CRC64;
Query Match 75.1%; Score 2810; DB 2; Length 546;
Best Local Similarity 98.3%; Pred. No. 4.6e-115;
Matches 525; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 17 KREKHPKPEPOOKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 76
Db 6 EKSSSERPEPOOKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 65
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QY 77 GGYHPVKIGDLFNGRYHYIRKLGWGHFSTVWLCWDMQGRFVAMKVKVSAQHYTETALDE 136
DB 66 GGYHPVKIGDLFNGRYHYIRKLGWGHFSTVWLCWDMQGRFVAMKVKVSAQHYTETALDE 125
QY 137 IKLLKCVRESPPSDPNKDMVQVLIIDDFKISGMNGIHVCMVFEVLGHHLLKWIISNYQGL 196
DB 126 IKLLKCVRESPPSDPNKDMVQVLIIDDFKISGMNGIHVCMVFEVLGHHLLKWIISNYQGL 185
QY 197 PVRVCSIIIRQVQLGDLVHSCCKIIHTDIKPENILMCDVDDAYVRRMAAEATEWQKAGAP 256
DB 186 PVRVCSIIIRQVQLGDLVHSCCKIIHTDIKPENILMCDVDDAYVRRMAAEATEWQKAGAP 245
QY 257 PPSGSAVSTAPOOKPIGKISKNKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 316
DB 246 PPSGSAVSTAPOOKPIGKISKNKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 305
QY 317 ITSAAPSNDQDGEYCPEVKLTGTTGLEAAAEATAKNGEAEDEQEKEDAEKENIEKDBDD 376
DB 306 ITSAAPSNDQDGEYCPEVKLTGTTGLEAAAEATAKNGEAEDEQEKEDAEKENIEKDBDD 365
QY 377 VDQELANIDPTWIESPKTNGHENGPFSLFSGSLFSGSLFSGSLFSGSLFSGSLFSGSLF 436
DB 366 VDQELANIDPTWIESPKTNGHENGPFSLFSGSLFSGSLFSGSLFSGSLFSGSLFSGSLF 425
QY 437 TYSSSYEQFNGELPNGRHKIPESQPFSTSLFSGSLFSGSLFSGSLFSGSLFSGSLFSGSLF 496
DB 426 TYSSSYEQFNGELPNGRHKIPESQPFSTSLFSGSLFSGSLFSGSLFSGSLFSGSLFSGSLF 485
QY 497 SHDRSRTVSASSTGDLPKAKTRAADLLVNPPLPRNADKIRVKIADLGNACVWHK 550
DB 486 SHDRSRTVSASSTGDLPKAKTRAADLLVNPPLPRNADKIRVKIADLGNACVWHK 539

RESULT 11
Q12890
ID Q12890 PRELIMINARY; PRT; 655 AA.
AC Q12890;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Serine kinase.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94268559; PubMed=8208298;
RA Gui J.F., Lane W.S., Fu X.D.;
RT "A serine kinase regulates intracellular localization of splicing
factors in the cell cycle [see comments].";
RL Nature 369:678-682(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RA Fu X.;
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: U09564; AAA20530.1; --
DR PIR: S45337; S45337.
DR HSP: Q03656; IHW.
DR GO: GO:0005634; C:nucleus; TAS.
DR GO: GO:0004672; P:protein kinase activity; TAS.
DR GO: GO:0000074; P:regulation of cell cycle; TAS.
DR GO: GO:0008380; P:RNA splicing; TAS.
DR InterPro: IPR011009; Kinase like.
DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser_Thr_pkin_AS.
DR Pfam: PF00069; Pkinase; 1.
DR ProDom: PD000001; Prot kinase; 2.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00101; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

SQ SEQUENCE 655 AA; 74319 MW; 7CDB98F0D2C16BD8 CRC64;
Query Match 55.3%; Score 2070.5; DB 2; Length 655;
Best Local Similarity 58.8%; Pred. No. 11e-82;
Matches 419; Conservative 84; Mismatches 133; Indels 77; Gaps 14;
QY 4 RKVLATQAKRR--PKREHPKPKPEQQAAPLVPVPPPPPPPPPPPPPPPPPPPPPPPPPP 61
DB 3 RKVLATQAKRR--PKREHPKPKPEQQAAPLVPVPPPPPPPPPPPPPPPPPPPPPPPPPP 49
QY 62 GSDDEQEDPADYCKGGYHPVKIGDLFNGRYHYIRKLGWGHFSTVWLCWDMQGRFVAMK 121
DB 50 GSDDEQEDPADYCKGGYHPVKIGDLFNGRYHYIRKLGWGHFSTVWLCWDMQGRFVAMK 109
QY 122 VKSAQHYTETALDEIKLLKCVRESPPSDPNKDMVQVLIIDDFKISGMNGIHVCMVFEVLG 181
DB 110 VKSAQHYTETALDEIKLLKCVRESPPSDPNKDMVQVLIIDDFKISGMNGIHVCMVFEVLG 169
QY 182 HLLKWIISKNYOGLPVRVCSIIIRQVQLGDLVHSCCKIIHTDIKPENILMCDVDDAYVRR 241
DB 170 HLLKWIISKNYOGLPVRVCSIIIRQVQLGDLVHSCCKIIHTDIKPENILMCDVDDAYVRR 229
QY 242 RMAAEATEWQKAGAPPPSGSAVSTAPOOKPIGKISKNKKKKKKKKKKKKKKKKKKKKKK 301
DB 230 RMAAEATEWQKAGAPPPSGSAVSTAPOOKPIGKISKNKKKKKKKKKKKKKKKKKKKKKK 289
QY 302 EELERAEERKIIIBENITSAAPSNDQDGEYCPEVKLTGTTGLEAAAEATAKNGEAEDEQ 361
DB 290 EEMEKES-----GPGQKRPNKQEESESPVERPL-----KENPPNKMTQE 328
QY 362 KEDAEKENIEKD-----EDVDQELANIDPTWIESPKTNGHENGPFSLFSGSLFSGSLF 416
DB 329 KLE-ESSTIGQDQTLMERDTTEGGAEEIN-----CNGVIE--VINYTONSNETLRHK 377
QY 417 EDCNPPEYNLDEPNAESDYTVSSSYEQFNGELPNGRHKIPESQPFSTSLFSGSLFSGSLF 476
DB 378 EDLHNDQVQNLNQESSFL-----SLPNGDSS--TSQETDSCPITSEVSDTM 425
QY 477 ACGSVLSEGSPLTEQESS-----PSHDSRTVSASSTGDLPKAKTRAADLLVNPPLPRN 526
DB 426 VCSSTVQGSFSGHISQLQESIRAEIPCEDEQ---EQEHNGFLDNKSGSTAGNLFVNP 482
QY 527 LDPRNADKIRVKIADLGNACVWHKFTEDIQTRYRSIEVLIGAGYSTPADINWSTACWAF 586
DB 483 LEPKNAEKLVKVIADLGNACVWHKFTEDIQTRYRSIEVLIGAGYSTPADINWSTACWAF 542
QY 587 ELATGDLVFEPSGDEYSDRDEHIAHIIELGSIIPRHFPALSGKYSRPFNRRGELRHITK 646
DB 543 ELATGDLVFEPSGDEYSDRDEHIAHIIELGSIIPRHFPALSGKYSRPFNRRGELRHITK 602
QY 647 LKPSLFDVLVEKYGWPHEDAAQFTDFELIMLEWVPEKRSAGSLRHPWLN 699
DB 603 LKPSLFDVLVEKYGWPHEDAAQFTDFELIMLEWVPEKRSAGSLRHPWLN 655

RESULT 12
Q96SB4
ID Q96SB4 PRELIMINARY; PRT; 826 AA.
AC Q96SB4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE SRPKla protein kinase.
GN Name=SRPK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21523916; PubMed=11509566;
RA Nikolaki E., Kohen R., Hartmann A.M., Stamm S., Georgatsou E.,
Giannakourou T.;

Db 54 DDEQEDNDYCKGYHHVKIGDLLNSKYHVRKLGWGHFSTVWLAWDIQGRFVAMKV 113
QY 124 KSAHYTETALDEIKLKVRESPPSPDNKVMVQLIDDFKISGMNGIHVCMFEVLGH 183
Db 114 KSAHYTETALDEIKLKVRESPPSPDNKVMVQLIDDFKISGMNGIHVCMFEVLGH 173
QY 184 LKWIISKYQGLPVRCKVSIIRQVGLDYLHSCKIIHTDIKPENILMCDVDDAYVRM 243
Db 174 LKWIISKYQGLPVRCKVSIIRQVGLDYLHSCKIIHTDIKPENILMCDVDDAYVRM 233
QY 244 AAEATEWOKAGAPPPSGSAVSTAPAPKQAPKMSKNKKKKKKQKRAELLEKRLQETEE 303
Db 234 AAEATEWOKAGAPPPSGSAVSTAPAPKQAPKMSKNKKKKKKQKRAELLEKRLQETEE 293
QY 304 LEREARKIIENITSAAPSDNDQGEYCPVVKLTGTLGEEAAEATAKDNGEADQEBKE 363
Db 294 MEIGPEGREEDD---DPESKPSCAP---LRQASLQETEE---TE 330
QY 364 DAENIKEDDDVDQELANIDPTWIESPKTNGHENGPFSLQQLDDEDD---E 416
Db 331 DIIMDTRELTSDASVEL-----NCGCLHS---SKTQPEDEQDLYGQLLQ 376
QY 417 EDCPNPEYNLDEPNAESDYTYSSYEQFNGELPNGRHKIPESQPFSTSLFSGSLPV 476
Db 377 EDHNN-----ANAGPETAQSMYECNG-----AESPELDQACYSNG---T 414
QY 477 ACGSVLSESGSPITEQEBSPPSHDRSRTVSASSTGDLPAKTRAAALLVNPDLPRNADKIR 536
Db 415 SQGEQLEDELATEEHOQKTRAREQNKIKD---DKLSAGSLVNPDLPLNADKIK 471
QY 537 VKIADLGNACWVHKHFTEDIQTRQVRSIEVLIGAGYSTPADITWSTACMAFELATGDYLFE 596
Db 472 VKIADLGNACWVHKHFTEDIQTRQVRSIEVLIGAGYSTPADITWSTACMAFELATGDYLFE 531
QY 597 PHSGEDYSRDEHIAHIIELLSGIPRHPALSGYSGRPPNRRGELRHITKLPWLSFDVL 656
Db 532 PHSGEDYSRDEHIAHIIELLSGIPRHPALSGYSGRPPNRRGELRHITKLPWLSFDVL 591
QY 657 VEKYGWPHEDAAQFTDFLIPMLEWPEKASAGECLRHHPWL 697
Db 592 MDKYEWPQEAQTFSDFLPMLLEPEKRAATAADCLRHHPWL 632

RESULT 14

AAH56825 PRELIMINARY; PRT; 634 AA.
ID AAH56825
AC AAH56825
DT 24-MAY-2004 (T-EMBLrel. 27, Created)
DT 24-MAY-2004 (T-EMBLrel. 27, Last sequence update)
DT 24-MAY-2004 (T-EMBLrel. 27, Last annotation update)
DE Hypothetical protein zgc:63789.
GN ZGC:63789.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RX Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056825; AAH56825.1; -;
KW Hypothetical protein.
SQ SEQUENCE 634 AA; 71712 MW; 95339BF0DB4B140D CRC64;

Query Match 55.1%; Score 2061; DB 2; Length 634;
Best Local Similarity 59.5%; Pred. No. 2.7e-82;
Matches 417; Conservative 71; Mismatches 135; Indels 78; Gaps 12;
QY 4 RKVLAIQARKRRPKREKHPKPEPQKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPEEEILGS 63
Db 3 RKVLAIQARKRRPKREKHPKPEPQKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPEEEILGS 53
QY 64 DDEQEDNDYCKGYHHVKIGDLLNSKYHVRKLGWGHFSTVWLAWDIQGRFVAMKV 123
Db 54 DDEQEDNDYCKGYHHVKIGDLLNSKYHVRKLGWGHFSTVWLAWDIQGRFVAMKV 113
QY 124 KSAHYTETALDEIKLKVRESPPSPDNKVMVQLIDDFKISGMNGIHVCMFEVLGH 183
Db 114 KSAHYTETALDEIKLKVRESPPSPDNKVMVQLIDDFKISGMNGIHVCMFEVLGH 173
QY 184 LKWIISKYQGLPVRCKVSIIRQVGLDYLHSCKIIHTDIKPENILMCDVDDAYVRM 243
Db 174 LKWIISKYQGLPVRCKVSIIRQVGLDYLHSCKIIHTDIKPENILMCDVDDAYVRM 233
QY 244 AAEATEWOKAGAPPPSGSAVSTAPAPKQAPKMSKNKKKKKKQKRAELLEKRLQETEE 303
Db 234 AAEATEWOKAGAPPPSGSAVSTAPAPKQAPKMSKNKKKKKKQKRAELLEKRLQETEE 293
QY 304 LEREARKIIENITSAAPSDNDQGEYCPVVKLTGTLGEEAAEATAKDNGEADQEBKE 363
Db 294 MEIGPEGREEDD---DPESKPSCAP---LRQASLQETEE---TE 330
QY 364 DAENIKEDDDVDQELANIDPTWIESPKTNGHENGPFSLQQLDDEDD---E 416
Db 331 DIIMDTRELTSDASVEL-----NCGCLHS---SKTQPEDEQDLYGQLLQ 376
QY 417 EDCPNPEYNLDEPNAESDYTYSSYEQFNGELPNGRHKIPESQPFSTSLFSGSLPV 476
Db 377 EDHNN-----ANAGPETAQSMYECNG-----AESPELDQACYSNG---T 414
QY 477 ACGSVLSESGSPITEQEBSPPSHDRSRTVSASSTGDLPAKTRAAALLVNPDLPRNADKIR 536
Db 415 SQGEQLEDELATEEHOQKTRAREQNKIKD---DKLSAGSLVNPDLPLNADKIK 471
QY 537 VKIADLGNACWVHKHFTEDIQTRQVRSIEVLIGAGYSTPADITWSTACMAFELATGDYLFE 596
Db 472 VKIADLGNACWVHKHFTEDIQTRQVRSIEVLIGAGYSTPADITWSTACMAFELATGDYLFE 531
QY 597 PHSGEDYSRDEHIAHIIELLSGIPRHPALSGYSGRPPNRRGELRHITKLPWLSFDVL 656
Db 532 PHSGEDYSRDEHIAHIIELLSGIPRHPALSGYSGRPPNRRGELRHITKLPWLSFDVL 591
QY 657 VEKYGWPHEDAAQFTDFLIPMLEWPEKASAGECLRHHPWL 697
Db 592 MDKYEWPQEAQTFSDFLPMLLEPEKRAATAADCLRHHPWL 632

RESULT 15
Q8IY12

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Db 424 TYSSYEQFNGELPNGQHTSEETPP-----LFGPLEFVACGVSISEGSLPTEQESSP 478
Qy 497 SHDRSRTVSAAGTGLPRAKTRAAADLLVNPDPNADKIRVKIADLGNACVWVHKHFTEDI 556
Db 479 SHDRSRTVSAAGTGLPXTKTRAAADLLVNPDPNADKIRVKIADLGNACVWVHKHFTEDI 538
Qy 557 QTRQVRSIEVLIGAGYSTPADIWSTACMAFELATGDYLFEPHSGSDYSRDEHDIAHIEL 616
Db 539 QTRQVRSIEVLIGAGYSTPADIWSTACMAFELATGDYLFEPHSGSDYSRDEHDIAHIEL 598
Qy 617 LGSIPRHAFALSGKYSREFFNRRGELRHITKLPWSLFDVLVEKYGWPHEDAAQFTDFLIP 676
Db 599 LGSIPRHAFALSGKYSREFFNRRGELRHITKLPWSLFDVLVEKYGWPHEDAAQFTDFLIP 658
Qy 677 MLEVPPEKRASAGECLRHPLWLS 699
Db 659 MLEVPPEKRASAGECLRHPLWLS 681

RESULT 2
S45337
serine protein kinase SRPK1 - human
C:Species: Homo sapiens (man)
C:Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S45337
R:Gui, J.F.; Lane, W.S.; Fu, X.D.
Nature 369, 678-682, 1994
A:Title: A serine kinase regulates intracellular localization of splicing factors in the
A:Reference number: S45337; PMID:8208298
A:Accession: S45337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-655 <GUI>
A:Cross-references: UNIPROT:Q12890; GB:U09564; NID:G507212; PIDN:AAA20530.1; PID:G507213

Query Match 55.3%; Score 2070.5; DB 2; Length 655;
Best Local Similarity 58.8%; Pred. No. 1.1e-87;
Matches 419; Conservative 84; Mismatches 133; Indels 77; Gaps 14;
Qy 4 RKVLAIQARKRR--PKREKHPKPPQOKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 61
Db 3 RKVLAIQARKKTKAKDKAQRKPTQHRG-----SAPHSESDLPEQEEL 49
Qy 62 GSDDEQEDPDADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCMDQGRFVAMK 121
Db 50 GSDDEQEDPDNDYCKGGYHLVKIGDLFNGRYHVIRKLGWGHFSTVWLSWDIQQKKFVAMK 109
Qy 122 VVKSQAHVTETALDEIKLLKCVRESDDPNKMDVQVLDLDPKISGMNGIHCWVFEVLG 181
Db 110 VVKSAEHYTETALDEIRLLKSVRNSDPNDPNEMVQVLLDDPKISGVNGTHICWVFEVLG 169
Qy 182 HLLKWIITKSNYQGLPVRCKVSIIRQVLQGLDYLHSCCKIHTDIPKPNILMCDVDDAYVR 241
Db 170 HLLKWIITKSNYQGLPVCVKIIQQVLQGLDYLHTRKRIHTDIPKPNILLVNEQYIR 229
Qy 242 RMAAEATEWQKAGAPPPSGSAVSTAPQOKPIGKISKNKKKLKKQKQKQAELEKRLQEI 301
Db 230 RLAAEATEWQSGAPPPSGSAVSTAPQPKADKMSKNKKKLKKQKQKQAELEKRMQEI 289
Qy 302 ELEREAEARKIIIEENITSAAPSDNDGECYCPVKLKTGTEEAABAEATAKNGEADQEE 361
Db 290 EEMEKES-----GPGQKRP-----KQKQKRP-----NKQEESEFVDRPLTENPN 328
Qy 362 KEDAKENIEKDDVDQELANIDPTWIESPKTNGHIE--NGPFSLEQQQLDDDD--DDE 416
Db 329 KLE-ESSTIGQQTLMERDEGAABIN-----CNGVIE--VINTQNSNNTLRHK 377
Qy 417 EDCPNPEYNLDEPNAESDYTYSSSYEQFNGELPGRHKIPESQPFSTSLFSGSLRPV 476
Db 378 EDLHNANDCDVQLNAQESSFL-----SLPNGDS--TSQETDSDCTPITSEVSDTM 425
Qy 477 ACGSVLSEGSPLTEQEES-----PSHRSRTVSAAGTGLP-KAKTRAAADLLVNP 526
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Db 426 VCQSSSTVGOSFSQHIISQLOESTRAEIPCEDEQ---EOEHNGFLDNKKGSTAGNFLVNP 482
Qy 527 LDPNADKIRVKIADLGNACVWVHKHFTEDIQTRQVRSIEVLIGAGYSTPADIWSTACMAF 586
Db 483 LEPKNAEKLKVKIADLGNACVWVHKHFTEDIQTRQVRSIEVLIGAGYSTPADIWSTACMAF 542
Qy 587 ELATGDYLFEPHSGSDYSRDEHDIAHIELLGSIPRHAFALSGKYSREFFNRRGELRHITK 646
Db 543 ELATGDYLFEPHSGSEETRDEHDIALIELLGVKPRKLIIVAGKYSKEFFTKKGLKHITK 602
Qy 647 LKPSLFDVLVEKYGWPHEDAAQFTDFLIPMLEVPEKRASAGECLRHPLWLS 699
Db 603 LKPMGLFEVLVEKYEQEAEANGFTDFLLPMLELIPKRRATAABCLRHPLWLS 655

RESULT 3
JC5930
serine/arginine-rich protein-specific kinase (EC 2.-.-.-) 1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: JC5930
R:Kuroyanagi, N.; Onogi, H.; Wakabayashi, T.; Hagiwara, M.
Biochem. Biophys. Res. Commun. 242, 357-364, 1998
A:Title: Novel SR-protein-specific kinase, SRPK2, disassembles nuclear speckles.
A:Reference number: JC5929; MUID:98113357; PMID:9446799
A:Accession: JC5930
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-648 <KUR>
A:Cross-references: UNIPROT:O70193; UNIPROT:O70551; UNIPROT:Q99J73
A:Experimental source: brain
C:Comment: This enzyme regulates the disassembly of the serine/arginine-rich proteins in
C:Keywords: transferase

Query Match 55.0%; Score 2058; DB 2; Length 648;
Best Local Similarity 57.7%; Pred. No. 3.9e-87;
Matches 414; Conservative 88; Mismatches 123; Indels 92; Gaps 13;
Qy 4 RKVLAIQARKRR--PKREKHPKPPQOKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 61
Db 3 RKVLAIQARKKTKAKDKAQRKPTQHRG-----SAPHSESDLPEQEEL 49
Qy 62 GSDDEQEDPDADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCMDQGRFVAMK 121
Db 50 GSDDEQEDPDNDYCKGGYHLVKIGDLFNGRYHVIRKLGWGHFSTVWLSWDIQQKKFVAMK 109
Qy 122 VVKSQAHVTETALDEIKLLKCVRESDDPNKMDVQVLDLDPKISGMNGIHCWVFEVLG 181
Db 110 VVKSAEHYTETALDEIRLLKSVRNSDPNDPNEMVQVLLDDPKISGVNGIHCWVFEVLG 169
Qy 182 HLLKWIITKSNYQGLPVRCKVSIIRQVLQGLDYLHSCCKIHTDIPKPNILMCDVDDAYVR 241
Db 170 HLLKWIITKSNYQGLPVCVKIIQQVLQGLDYLHTRKRIHTDIPKPNILLVNEQYIR 229
Qy 242 RMAAEATEWQKAGAPPPSGSAVSTAPQOKPIGKISKNKKKLKKQKQKQAELEKRLQEI 301
Db 230 RLAAEATEWQSGAPPPSGSAVSTAPQPKADKMSKNKKKLKKQKQKQAELEKRMQEI 289
Qy 302 ELEREAEARKIIIEENITSAAPSDNDGECYCPVKLKTGTEEAABAEATAKNGEADQEE 361
Db 290 EEMEKES-----GPGQKRP-----NKQEESEFVDRPLTENPN 323
Qy 362 KEDAKENIEKDDVDQELANIDPTWIESPKTNGHIE--NGPFSLEQQQLDDDD--DDE 415
Db 324 KWTQEK---LEBSNIGQ---DQTLTERGEGGAPEINCNGVIGVVVNPENSNNETLR 375
Qy 416 -EDCPNPEYNLDEPNAESDYTYSSSYEQFNGELPGRHKIPESQPFSTSLFSGSLE 474
Db 376 HKEDLHNANDCDVHTLKQEPSFLNS-----NG-----DSSPQSDTDSCT 415
Qy 475 PVACGSVLSEGS-----PLTQEEES-----PSHRSRTVSAAGTGLPKAKTRAAADL 522
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Db 416 PTASFTVWCSSAEQSLTRQDITQLBESIRADTPSPGDEQPNGLDSDS-----KGKFSAGNF 471
Qy 523 LVNPLDPRNADKIRVKIADLGNACVWVKHFTEDIQTRQVRSIEVLIGAGYSTPADIWSTA 582
Db 472 LINPLEPKNAELQVKIADLGNACVWVKHFTEDIQTRQVRSIEVLIGAGYSTPADIWSTA 531
Qy 583 CMAFELATGDYLFEPHSGSDYSDRDEHIAHIELLGSIPRHPALSGKYSREFNRRGELR 642
Db 532 CMAFELATGDYLFEPHSGSDYTRDEHIAHIELLGVKPKLIVAGKYSKEFTTKGDDUK 591
Qy 643 HITKLPWSLFDVLVEKYGMPHEDAAQFTDFLIPMLEMVPKRSASAGECLRHPLWNS 699
Db 592 HITKLPWGLLEVLVEKYGMPQEEAAGFTDFLLPMLPELMPEKRAATAECLRHPLWNS 648
RESULT 4
S28282
hypothetical protein B0464.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
C:Accession: S28282
R:Kershaw, J.
submitted to the EMBL Data Library, December 1992
A:Reference number: S28278
A:Accession: S28282
A:Molecule type: DNA
A:Residues: 1-1087 <KER>
A:Cross-references: UNIPROT:Q03563; EMBL:Z19152
C:Genetics:
A:Introns:
C:Keywords: serine/threonine-specific protein kinase
Query Match 36.7%; Score 1374; DB 2; Length 1087;
Best Local Similarity 46.7%; Pred. No. 1.3e-55;
Matches 305; Conservative 68; Mismatches 158; Indels 122; Gaps 13;
Qy 53 PPEPEEILGSDDEQEDPADYCKGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCDWM 112
Db 481 PMPDGEQ-LGSDDEQEDPRDYKRGYHPVNIQGVFNARYHVIRKLGWGHFSTVWLAWDT 539
Qy 113 QOKRFVAMKVKSAOHHYETALDEIKLLKCVRESPPSPDKMVKVQLIDDFKISGMNGIH 172
Db 540 QOKRFVAMKVKSAHYTEALDEIKLLSVRSADPNDIGCHVKVQLLDFEFTVGTINGQH 599
Qy 173 VCMVEVLGHLLKWIISNYOGLPVRVKSIIROVLQGLDYLSHCKKIIHTDIKPENIL 232
Db 600 VAMVEVLGCNLLKLIIRSNYRGLHLEQVRKICQVLEALGYMHEKCGIIHTDIKPENVL 659
Qy 233 MCVDDAYVRRMAAEATEWQKAGAPPSPGSASVTAPO---QKPIGKISKNKKKKKKKK 289
Db 660 ITMSREEIKMAQHAVVARKNM-KMSGSAVSTAPDHLVYKMAQENNTKNNKKKKKKK 718
Qy 290 QALLLEKRLQEIIEELEREAEKIIENITSAAPSNDQDGEYCPEVKLKTTLGLEAAEAE 349
Db 719 QREKLEAELAGLEGLKWDANG--LQAYNNAPLTNIGKYSMCMNNGTLELNF----- 771
Qy 350 AKDNGEADQERKEDAEKENIEKDEDDVDQELANIDPTWIESPKTNGHIENGPFSLQOL 409
Db 772 ---NASQVEDVTMEDVTNEN-----GNRNKVEIRSPDRFDTTLTPFS----- 811
Qy 410 DDEDDDEECNPPEY--NLDEPNABSDTYSSSYEQFNGELPNGRHKIPESQPFESTS 467
Db 812 -----DPESKFGDLASPSAE-----YLSS-----PMSQLP----- 836
Qy 468 LFGSLPEPVACGVLSEGSPLTEQESSPSHDSRTVSASTGDLPAKTRAADLLVNL 527
Db 837 ---PGILPAP-----PV 846
Qy 528 DPNAD---KIRVKIADLGNACVWVKHFTEDIQTRQVRSIEVLIGAGYSTPADIWSTA 584
Db 847 GPNIGDPYCIDVKIADLGNACVWVNHHTDDIQTRQVRALEVLIGSGYGPADIWSTA 906
Qy 585 AFELATGDYLFEPHSGSDYSDRDEHIAHIELLGSIPRHPALSGKYSREFNRRGELRH 644

Db 907 AFELATGDYLFEPHOGDNYSRDEDLAHISELLGAIPPSIYKKGKRWRFEPHNGHLLHI 966
Qy 645 TIKLPWSLFDVLVEKYGMPHEDAAQFTDFLIPMLEMVPKRSASAGECLRHPLW 697
Db 967 HQLKWSLVEVLQVKYEWSHEDAQFESFLRPMWLDQDEKSTAKIALKHPFL 1019
RESULT 5
F88556
protein B0464.5a [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F88556
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:9069613; PMID:9851916
A>Note: see website genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: F88556
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1093 <STO>
A:Cross-references: UNIPROT:Q03563; GB:chr_III; PIDN:CAA79540.1; PID:g3873796; GSPDB:GN
C:Genetics:
A:Gene: B0464.5a
A:Map position: 3
Query Match 36.7%; Score 1374; DB 2; Length 1093;
Best Local Similarity 46.4%; Pred. No. 1.4e-55;
Matches 304; Conservative 64; Mismatches 143; Indels 144; Gaps 13;
Qy 53 PPEPEEILGSDDEQEDPADYCKGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCDWM 112
Db 481 PMPDGEQ-LGSDDEQEDPRDYKRGYHPVNIQGVFNARYHVIRKLGWGHFSTVWLAWDT 539
Qy 113 QOKRFVAMKVKSAOHHYETALDEIKLLKCVRESPPSPDKMVKVQLIDDFKISGMNGIH 172
Db 540 QOKRFVAMKVKSAHYTEALDEIKLLSVRSADPNDIGCHVKVQLLDFEFTVGTINGQH 599
Qy 173 VCMVEVLGHLLKWIISNYOGLPVRVKSIIROVLQGLDYLSHCKKIIHTDIKPENIL 232
Db 600 VAMVEVLGCNLLKLIIRSNYRGLHLEQVRKICQVLEALGYMHEKCGIIHTDIKPENVL 659
Qy 233 MCVDDAYVRRMAAEATEWQKAGAPPSPGSASVTAPO---QKPIGKISKNKKKKKKKK 289
Db 660 ITMSREEIKMAQHAVVARKNM-KMSGSAVSTAPDHLVYKMAQENNTKNNKKKKKKK 718
Qy 290 QALLLEKRLQEIIEELEREAEKIIENITSAAPSNDQDGEYCPEVKLKTTLGLEAAEAE 349
Db 719 QREKLEAELAGLEGLKWDANG--LQAYNNAPLTNIGKYSMCMNNGTLELNF----- 771
Qy 350 AKDNGEADQERKEDAEKENIEKDEDDVDQELANIDPTWIESPKTNGHIENGPFSLQOL 407
Db 749 ELENENASQVEDVTMEDVTNEN-----GNRNKVEIRSPDRFDTTLTPFS----- 793
Qy 408 QLDDDDDEECNPPEY--NLDEPNABSDTYSSSYEQFNGELPNGRHKIPESQPFESTS 465
Db 794 -----DPESKFGDLASPSAE-----YLSS-----PMSQLP----- 818
Qy 466 TSLFGSLPEPVACGVLSEGSPLTEQESSPSHDSRTVSASTGDLPAKTRAADLLVNL 525
Db 819 ----PGILPAP----- 826
Qy 526 PLDPNAD---KIRVKIADLGNACVWVKHFTEDIQTRQVRSIEVLIGAGYSTPADIWSTA 582
Db 827 PVPNGIDPYCIDVKIADLGNACVWVNHHTDDIQTRQVRALEVLIGSGYGPADIWSTA 886
Qy 583 CMAFELATGDYLFEPHSGSDYSDRDEHIAHIELLGSIPRHPALSGKYSREFNRRGELR 642
Db 887 CMAFELATGDYLFEPHOGDNYSDRDEDLAHISELLGAIPPSIYKKGKRWRFEPHNGHLL 946

QY	516	K-----	516
DB	597	KYPNSNDVYKPEKDINKPPIYCDMPNHLIHPREALRLHLYMKNKNIDSNNTMDLGN	556
QY	517	-----TRAADLLVNLDPDR--NADKIRVKIADLGNACVHKKFTEDIQTRYRSI	564
DB	657	QNSHKVYINTDEGEYCIRPDPSPVYVYHEKSCVKICDLGNSLWIDBSRVAEIQRYRAP	716
QY	565	EVILGAGYSTPADINSTACWAFELATGDYLFEPHSGEDYSRDEDHIAHIELLSIPRHF	624
DB	717	EVILSGGFNETADISFACWAFELVTGDFLFPQKGRDYDKNEEHLSPFIEVLGNIPKHM	776
QY	625	ALSGKYSRFFNRG-ELRHITKLKPSLFDVLVEKYGWPHEDAAQFTDFLIPMLEMVE	683
DB	777	IDAGYNSHKYFNKNVYLNIRNKKYGLYKILKYKYNLPEKISPLCSFLPMLSVDPQ	836
QY	684	KRASAGECLRHFWLN	698
DB	837	TRPSAYTMLQHPWLN	851
RESULT 12			
C84553			
probable protein kinase [imported] - Arabidopsis thaliana			
C:Species: Arabidopsis thaliana (mouse-ear cress)			
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004			
C:Accession: C84553			
R:Lin, X.; Kaul, S.; Rounleay, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;			
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.			
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.			
Nature 402, 761-768, 1999			
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.			
A:Reference numbers: A84420; MUID:20083487; PMID:10617197			
A:Accession: C84553			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-440 <STO>			
A:Cross-references: UNIPROT:Q9SHL5; GB:AE002093; NID:G4914374; PIDN:AAD32910.1; GSPDB:GN			
C:Genetics:			
A:Gene: At2g17530			
A:Map position: 2			
C:Superfamily: human protein kinase clkl; protein kinase homology			
Query Match 22.4%; Score 838; DB 2; Length 440;			
Best Local Similarity 30.3%; Pred. No. 1.5e-31;			
Matches 194; Conservative 78; Mismatches 133; Indels 236; Gaps 11;			
QY	63	SDDEQEDPAD-YCKGGYHPVKIGDLF-NGRYHVIRKLGWGHFSTVWLCMDMQGRFVAM	120
DB	7	SGSEDDDEGFDAYRKGGYHVRIGDQFAGGRVIAQRKLGWGFSTVWLAIDRTSNYVAL	66
QY	121	KVKSQAQHYTETALDEIKLLKCVRESDDPNKDMVVQLIDDFKISGMNGIHVCWVFEVL	180
DB	67	KIQSALQPAQAALHEILLQAAADGPE--NTKCVIRLIDDFKHAGPNGQHLWVLEFL	124
QY	181	GHHLLKWIKNYQGLPVCVKSIIQVLOGLDYLHSCKIIHTDIKPENILMC--VDDA	238
DB	125	GDSLLRLIKYNYKGMELSKVREICKILTGDLHRELGMHSDLKPENILLCSTID--	182
QY	239	YVRRMAAEATEKQACAPPSAVSTAPQKPIKISKNK-KKKLKKQKQKQALKEK	297
DB	183	-----PAKQPIRSGLT-----ILEKPEGNQNGTSTWNLEKLLKRAKAAAKISGR	230
QY	298	LOEIELEAREARKIIEENITSAAPSDNDGECYCEVKLTGLEEAAREATAKONGAE	357
DB	231	-----RVSIVGLS-----	238
QY	358	DOEKEDAEKENIEKDDVDQELANIDPTWIESPKTNGHIENGPFSLQQLDDDEE	417
DB	239	-----ETPKKN-----	252
QY	418	DCPNPEYNLDEPNAESDYSSSYEQFNGELPNGRHKIPESQPFSTSLFSGSL	477

DB	253	-----	252
QY	478	CGSVLSEGSPLTEQESSPSHDSRTVSASSTGDLPLKAKTRAADLLVNLDPNRADKIRV	537
DB	253	-----	255
QY	538	KIADLGNACVHKKHFTEDIQTRYRSIEVLGAGYSTPADINSTACWAFELATGDYLFEP	597
DB	256	KVVDGNGCWADNKFABEIQTRYRAPEVILQSGYSYSDVMMSFACTAFELATGDMFLFAP	315
QY	598	HSGEDYSRDEDHIAHIELLSIPRHFALSGYKSYREFFNRRGELRHITKLKWSLFDVLV	657
DB	316	KEGNGYGEDEHIALMMLLGMKPKIAIGGARSXDYFDRHGLDKRIIRLYKWPFLDLRI	375
QY	658	EKYGPHFHDAQAQFTDFLIPMLEMVEPKASAGECLRHFWLN	698
DB	376	DYKLPFAEAREFADFLCPIMDFAPEKRPPTAQOCLQHPWLN	416
RESULT 13			
T04655			
protein kinase homolog F8D20.10 - Arabidopsis thaliana			
C:Species: Arabidopsis thaliana (mouse-ear cress)			
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004			
C:Accession: T04655			
R:Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.; Vos, P.; Mewes			
submitted to the Protein Sequence Database, July 1998			
A:Reference number: Z15381			
A:Molecule type: DNA			
A:Residues: 1-438 <BEV>			
A:Cross-references: UNIPROT:O81783; EMBL:AL031135			
A:Experimental source: cultivar Columbia; BAC clone F8D20			
C:Genetics:			
A:Map position: 4			
A:Introns: 61/3; 326/3; 342/3			
A:Note: F8D20.10			
C:Superfamily: human protein kinase clkl; protein kinase homology			
Query Match 22.3%; Score 834.5; DB 2; Length 438;			
Best Local Similarity 31.3%; Pred. No. 2.2e-31;			
Matches 202; Conservative 71; Mismatches 129; Indels 243; Gaps 13;			
QY	62	GSDDEQEDPADYCKGGYHPVKIGDLFN-GRYHVIRKLGWGHFSTVWLCMDMQGRFVAM	120
DB	8	SGSEEGGFDA-YRKGGYHVRIGDPSGGRVIAQRKLGWGFSTVWLAIDTLTSTVAL	66
QY	121	KVKSQAQHYTETALDEIKLLKCVRESDDPNKDMVVQLIDDFKISGMNGIHVCWVFEVL	180
DB	67	KIQSQAQPAQAALHEIFLSAAADGD-LDKTK-CVRLIDHFKHSGPNGQHLWVLEFL	124
QY	181	GHHLLKWIKNYQGLPVCVKSIIQVLOGLDYLHSCKIIHTDIKPENILMC--VDDA	238
DB	125	GDSLLRLIKYNYQGLKLVKREICRCILTGDLHRELGMHSDLKPENILLCSTID--	182
QY	239	YVRRMAAEATEKQACAGAPP-----PGSAVSTAPQKPIKISKNKKKKKKQKQKQ-AEL	293
DB	183	-----PAKQPVRSGLTPLLEKPEGNANGASTWNLI-----EKKLKRRAKRAVAKI	228
QY	294	LEKRLQETEELEAREARKIIEENITSAAPSDNDGECYCEVKLTGTTGLEEAAREATAKON	353
DB	229	SERRVSMV-----	245
QY	354	GEAQDEBEKDAEKENIEKDDVDQELANIDPTWIESPKTNGHIENGPFSLQQLDDDED	413
DB	246	-----EKSLDGID-----	253
QY	414	DDEDCPNPEYNLDEPNAESDYSSSYEQFNGELPNGRHKIPESQPFSTSLFSGSL	473
DB	254	-----	253
QY	474	EPVACGSVLSEGSPLTEQESSPSHDSRTVSASSTGDLPLKAKTRAADLLVNLDPNRAD	533


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QY 283 LKKKQKRAELLEKLQIELELEERAERKIIIEENITSAAPSDQDQGYCPEVKLKTGLE 342
Db 205 -----VSSENV----- 210
QY 343 EAAEAETAKNGEAEQOEKDAEKENIEKDEDDVDQELANIDPTWIESPKTNCHIENGP 402
Db 211 ----- 210
QY 403 FSLEQOQDDEDEDCPNPEYNILDEPNAESDYTYSSSYEOFNGELPNGRHKIPESOPP 462
Db 211 -----KLPDN--- 215
QY 463 EFSTSLFSGSLPEVACGVLSEGSPLTEQESSPSGHRDRTVSASSTGDLPAKTRAADL 522
Db 216 -----KRSAAETHFRC-----LPKSSA----- 233
QY 523 LVNPLDPRNADKIRVKIADLGNACWVHKHFTEDIOIOTQYRSIEVLIGAGYSTPADIWSTA 582
Db 234 -----IKLIDFGSTVCNRIHHSIVQTRHYRSPDEVILGLWSYQCDLWSIG 279
QY 583 CMAFELATGYLFEPHSGEDYSRDEHDIAHIIELGSIPIRHPALSGKYSREFFNRRG--- 639
Db 280 CILFELCTGEALFQTHD-----NLEHLAMMERALGPLPEHMTKASRGAEKYFRGCGRL 333
QY 640 -----ELRHITKLPWSLFDVLVEKYCWPHED--AAQFTDPLIPMLEWVPEK 684
Db 334 NWPEGANSRESIRAVKRLDRLKD-----MVSK-----HVDNTRSRFADLLYGLLAYDPSE 383
QY 685 RASAGECLRHPPWLS 699
Db 384 RLTAENEALDHPFFKS 398

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Search completed: January 19, 2005, 15:41:35
Job time : 49 secs

...uge Blank (uspio)

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3742	100.0	699	9	US-09-759-359A-2	Sequence 2, Appli
2	3742	100.0	699	14	US-10-207-973-2	Sequence 2, Appli
3	3742	100.0	699	16	US-10-699-676-2	Sequence 2, Appli
4	3626	96.9	688	17	US-10-618-941-102	Sequence 102, Appli
5	3614	96.6	715	15	US-10-425-114-4382	Sequence 54382, Appli
6	3586	95.8	686	10	US-09-981-397A-22	Sequence 22, Appli
7	2070.5	55.3	655	14	US-10-116-275-142	Sequence 142, Appli
8	1862	50.3	533	14	US-10-353-690-48	Sequence 48, Appli
9	1882	50.3	533	17	US-10-723-860-1549	Sequence 1549, Appli
10	1374	36.7	698	14	US-10-369-493-5839	Sequence 5839, Appli
11	1364.5	36.5	782	14	US-10-369-493-5838	Sequence 5838, Appli
12	1076.5	28.8	550	15	US-10-425-114-49483	Sequence 49483, Appli
13	1071.5	28.6	547	15	US-10-424-599-215731	Sequence 215731, Appli

QY 181 GHLLKWIISKYQGLPVRCKVSIIRVQLQGLDYLSKCKIIHTDIKPENILMCVDDAYV 240
DB 181 GHLLKWIISKYQGLPVRCKVSIIRVQLQGLDYLSKCKIIHTDIKPENILMCVDDAYV 240
QY 241 RMAAEATEWOKAGAPPSGSAVSTAPQOKPIGKISKNKKKKLKKQKQKQAELEKRLQ 300
DB 241 RMAAEATEWOKAGAPPSGSAVSTAPQOKPIGKISKNKKKKLKKQKQKQAELEKRLQ 300
QY 301 IEELEREAEKRIIEENITSAAPSNDQDGEYCPEVKLKTTLGLEAAAEATAKDNGBAEDQ 360
DB 301 IEELEREAEKRIIEENITSAAPSNDQDGEYCPEVKLKTTLGLEAAAEATAKDNGBAEDQ 360
QY 361 EKEDAENIEKDEDDVDQELANIDPTWIESPKTNHNGIENGPFSLQQLDDDEDEDCP 420
DB 361 EKEDAENIEKDEDDVDQELANIDPTWIESPKTNHNGIENGPFSLQQLDDDEDEDCP 420
QY 421 NPEEYNLDEPNAESDYTYSSSYEQNGELPNGRHKIPESQPFPESTSLFSGSLEPVACGS 480
DB 421 NPEEYNLDEPNAESDYTYSSSYEQNGELPNGRHKIPESQPFPESTSLFSGSLEPVACGS 480
QY 481 VLSEGSPLTEQESPSHDSRTVSASSTGDLPAKTRAADLLVNPLDPRNADKIRVKIA 540
DB 481 VLSEGSPLTEQESPSHDSRTVSASSTGDLPAKTRAADLLVNPLDPRNADKIRVKIA 540
QY 541 DLGNACVWHKHTEDIOTRQYRSIEVLIGAGYSTPADIWSTACMAFELATGDLPEPHSG 600
DB 541 DLGNACVWHKHTEDIOTRQYRSIEVLIGAGYSTPADIWSTACMAFELATGDLPEPHSG 600
QY 601 EDYSRDEDHIAHIELLGSIPRHFAISGKYSREFFNRGELRHITKLPWSLFDVLVVKY 660
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QY 661 GMPHEDAAQFTDFLIPMLEMVEPKASAGECLRHPLWLS 699
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RESULT 2

US-10-207-973-2
; Sequence 2, Application US/10207973
; Publication No. US20030175927A1
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/10/207,973
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Human
US-10-207-973-2

Query Match 100.0%; Score 3742; DB 14; Length 699;
Best Local Similarity 100.0%; Pred. No. 9,6e-198;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSRKVLAIQAKRRPKREKHPKPEQOKAPLVPPPPPPPPPPPPPPPPPPPPPPPP 60
DB 1 MSSRKVLAIQAKRRPKREKHPKPEQOKAPLVPPPPPPPPPPPPPPPPPPPPPPPP 60
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DB 61 LGSDEDEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCWDMQGRFVAM 120
QY 121 KVVSAQHYTETALDEIKLLKCVRESDDPSDPNKMVVQLIDDFKISGMNGIHCVMVFEVL 180
DB 121 KVVSAQHYTETALDEIKLLKCVRESDDPSDPNKMVVQLIDDFKISGMNGIHCVMVFEVL 180

QY 181 GHLLKWIISKYQGLPVRCKVSIIRVQLQGLDYLSKCKIIHTDIKPENILMCVDDAYV 240
DB 181 GHLLKWIISKYQGLPVRCKVSIIRVQLQGLDYLSKCKIIHTDIKPENILMCVDDAYV 240
QY 241 RMAAEATEWOKAGAPPSGSAVSTAPQOKPIGKISKNKKKKLKKQKQKQAELEKRLQ 300
DB 241 RMAAEATEWOKAGAPPSGSAVSTAPQOKPIGKISKNKKKKLKKQKQKQAELEKRLQ 300
QY 301 IEELEREAEKRIIEENITSAAPSNDQDGEYCPEVKLKTTLGLEAAAEATAKDNGBAEDQ 360
DB 301 IEELEREAEKRIIEENITSAAPSNDQDGEYCPEVKLKTTLGLEAAAEATAKDNGBAEDQ 360
QY 361 EKEDAENIEKDEDDVDQELANIDPTWIESPKTNHNGIENGPFSLQQLDDDEDEDCP 420
DB 361 EKEDAENIEKDEDDVDQELANIDPTWIESPKTNHNGIENGPFSLQQLDDDEDEDCP 420
QY 421 NPEEYNLDEPNAESDYTYSSSYEQNGELPNGRHKIPESQPFPESTSLFSGSLEPVACGS 480
DB 421 NPEEYNLDEPNAESDYTYSSSYEQNGELPNGRHKIPESQPFPESTSLFSGSLEPVACGS 480
QY 481 VLSEGSPLTEQESPSHDSRTVSASSTGDLPAKTRAADLLVNPLDPRNADKIRVKIA 540
DB 481 VLSEGSPLTEQESPSHDSRTVSASSTGDLPAKTRAADLLVNPLDPRNADKIRVKIA 540
QY 541 DLGNACVWHKHTEDIOTRQYRSIEVLIGAGYSTPADIWSTACMAFELATGDLPEPHSG 600
DB 541 DLGNACVWHKHTEDIOTRQYRSIEVLIGAGYSTPADIWSTACMAFELATGDLPEPHSG 600
QY 601 EDYSRDEDHIAHIELLGSIPRHFAISGKYSREFFNRGELRHITKLPWSLFDVLVVKY 660
DB 601 EDYSRDEDHIAHIELLGSIPRHFAISGKYSREFFNRGELRHITKLPWSLFDVLVVKY 660
QY 661 GMPHEDAAQFTDFLIPMLEMVEPKASAGECLRHPLWLS 699
DB 661 GMPHEDAAQFTDFLIPMLEMVEPKASAGECLRHPLWLS 699

RESULT 3

US-10-799-676-2
; Sequence 2, Application US/10799676
; Publication No. US20040157297A1
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001043DIV II
; CURRENT APPLICATION NUMBER: US/10/799,676
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: 10/207,973
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 09/759,359
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-799-676-2

Query Match 100.0%; Score 3742; DB 16; Length 699;
Best Local Similarity 100.0%; Pred. No. 9,6e-198;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSRKVLAIQAKRRPKREKHPKPEQOKAPLVPPPPPPPPPPPPPPPPPPPPPPPP 60
DB 1 MSSRKVLAIQAKRRPKREKHPKPEQOKAPLVPPPPPPPPPPPPPPPPPPPPPPPP 60
QY 61 LGSDEDEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCWDMQGRFVAM 120
DB 61 LGSDEDEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCWDMQGRFVAM 120

Qy	121	KVKSAQHYTETALDEIKLLKCVRESDDSDPNKMVQVLIIDDFKISGNGIHCVMVFVL	180
Db	121	KVKSAQHYTETALDEIKLLKCVRESDDSDPNKMVQVLIIDDFKISGNGIHCVMVFVL	180
Qy	181	GHLLKWIILKSNYQGLPVCVKSIIRQVLQGLDYLHSCCKLIHTDIKBPENILCMCVDVAV	240
Db	181	GHLLKWIILKSNYQGLPVCVKSIIRQVLQGLDYLHSCCKLIHTDIKBPENILCMCVDVAV	240
Qy	241	RRMAAEATEWQACAGAPPSGAVSTAPOQKPIGKISKNKKKLLKKKQKQRAELLEKRLOE	300
Db	241	RRMAAEATEWQACAGAPPSGAVSTAPOQKPIGKISKNKKKLLKKKQKQRAELLEKRLOE	300
Qy	301	IEELERAERKII BENITSAAPSDQGEYCPEVKLKTGGLSEAAEAETAKDNGEAEQOE	360
Db	301	IEELERAERKII BENITSAAPSDQGEYCPEVKLKTGGLSEAAEAETAKDNGEAEQOE	360
Qy	361	EKEDAEKENIEKDEDDVDQELANIDPTWIESPKTNGHTIENGPFSLQQLDDDEDDDEDCP	420
Db	361	EKEDAEKENIEKDEDDVDQELANIDPTWIESPKTNGHTIENGPFSLQQLDDDEDDDEDCP	420
Qy	421	NPEEYNLDEPNAESDYTYSSSYEOFNGLPNGRHKI PESQPEFSTSLFSGSLEPVACGS	480
Db	421	NPEEYNLDEPNAESDYTYSSSYEOFNGLPNGRHKI PESQPEFSTSLFSGSLEPVACGS	480
Qy	481	VLSEGSPLTEQEESSPSHDSRTVSAASGTGLPKAKTRAADLLVNNPLDPRNADKIRVKIA	540
Db	481	VLSEGSPLTEQEESSPSHDSRTVSAASGTGLPKAKTRAADLLVNNPLDPRNADKIRVKIA	540
Qy	541	DLGNACVWHKHFTEDIQTRQYSIEVLGAGYSTPADIWSTACMAFELATGDYLFEPHSG	600
Db	541	DLGNACVWHKHFTEDIQTRQYSIEVLGAGYSTPADIWSTACMAFELATGDYLFEPHSG	600
Qy	601	EDYSRDEDHIAHII TELGSI PRHFALSGKYSREFFNRNGELRHITKLPWSLFDVLVEKY	660
Db	601	EDYSRDEDHIAHII TELGSI PRHFALSGKYSREFFNRNGELRHITKLPWSLFDVLVEKY	660
Qy	661	GWPHEDAAQFTDFLIPMLEMVPKXASAGECLRHPPWLS	699
Db	661	GWPHEDAAQFTDFLIPMLEMVPKXASAGECLRHPPWLS	699
RESULT 4			
US-10-618-941-102			
; Sequence 102, Application US/10618941			
; Publication No. US20040197792A1			
; GENERAL INFORMATION:			
; APPLICANT: WHYTE, DAVID			
; APPLICANT: MANNING, GERARD			
; APPLICANT: CAENEPEEL, SEAN			
; TITLE OF INVENTION: NOVEL KINASES			
; FILE REFERENCE: 034536-0321			
; CURRENT APPLICATION NUMBER: US/10/618,941			
; CURRENT FILING DATE: 2003-07-15			
; PRIOR APPLICATION NUMBER: 60/395,632			
; PRIOR FILING DATE: 2002-07-15			
; NUMBER OF SEQ ID NOS: 143			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 102			
; LENGTH: 688			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-618-941-102			

Query Match 96.9%; Score 3626; DB 17; Length 688;
Best Local Similarity 98.8%; Pred. No. 2.3e-191;
Matches 675; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy	17	KREHKPKGEPOQAKPLVPPPPPPPPPPPLPDTPTPEPEEEILGSDDEQEEDPADYCK	76
	:	:	
Db	6	EKSSSERPEQOQAKPLVPPPPPPPPPPPLPDTPTPEPEEEILGSDDEQEEDPADYCK	65
Qy	77	GGYHPVKIGDLFNGRVHVIRKLGWGHFSTVWLCDWMOGKRFAMKVKSQAHYTTETALDE	136

Db	66	GGYHPVKIGDLFNFGRYHVIRKLGNGHSTVWLCWDMQKGRFVAMKVKSQAQHYTETALDE	125
Qy	137	IKLLKCVRESDPSPDNKMVYQLIDDFKISGMNGIHVCWPEVLGHLLKWIISKNSYQGL	196
Db	126	IKLLKCVRESDPSPDNKMVYQLIDDFKISGMNGIHVCWPEVLGHLLKWIISKNSYQGL	185
Qy	197	PVRCVKSIIRQVLQGLDYLHSKCKIIHTDIIKPENILMCVDDAYVRRMAAEATEWOKAGAP	256
Db	186	PVRCVKSIIRQVLQGLDYLHSKCKIIHTDIIKPENILMCVDDAYVRRMAAEATEWOKAGAP	245
Qy	257	PPSGSVASTPAQOQPIGKISNKKKKLKKKQKQAELEKRLQELTEELEREAEERKIIIEEN	316
Db	246	PPSGSVASTPAQOQPIGKISNKKKKLKKKQKQAELEKRLQELTEELEREAEERKIIIEEN	305
Qy	317	ITSAAPSNQDGEYCPEVKLKTITGLEEAAAEATAKNGEAEDEQEKEDAENIKEDEDD	376
Db	306	ITSAAPSNQDGEYCPEVKLKTITGLEEAAAEATAKNGEAEDEQEKEDAENIKEDEDD	365
Qy	377	VDQELANIDPTWIESPKTNGHIENGPSLEQOOLDDEDDDEDCPNPEYNLDEPNAESDY	436
Db	366	VDQELANIDPTWIESPKTNGHIENGPSLEQOOLDDEDDDEDCPNPEYNLDEPNAESDY	425
Qy	437	TYSSSYEQFNGELPNGRHKHIPESQPPFSTSLFGSLPEPVACGSLSEGSPLTEQEBESSP	496
Db	426	TYSSSYEQFNGELPNGRHKHIPESQPPFSTSLFGSLPEPVACGSLSEGSPLTEQEBESSP	485
Qy	497	SHDSRSTVSASSTGDLPAKTRAADLLVNPJDPNNADKIRVKIADLGNACWVHKHFTEDI	556
Db	486	SHDSRSTVSASSTGDLPAKTRAADLLVNPJDPNNADKIRVKIADLGNACWVHKHFTEDI	545
Qy	557	QTROYSRIEVLIGAGYSTPADIWSTACWAFELATGDYLFEPHSGSGEDYSRDEDHIAHIEL	616
Db	546	QTROYSRIEVLIGAGYSTPADIWSTACWAFELATGDYLFEPHSGSGEDYSRDEDHIAHIEL	605
Qy	617	LGS1PRHFALSGKYSRFFFNRRRGE1RHITKLKPNWSLFDVLVEKYGWPHDEAAQOFTDFLLP	676
Db	606	LGS1PRHFALSGKYSRFFFNRRRGE1RHITKLKPNWSLFDVLVEKYGWPHDEAAQOFTDFLLP	665
Qy	677	MLEMVPEKRASAGECLRHFWLNS	699
Db	666	MLEMVPEKRASAGECLRHFWLNS	688

RESULT 5

```

US-10-425-114-54382
; Sequence 54382, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54382
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3063-134-E5_FLI.pep
US-10-425-114-54382

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Query Match          96.6%; Score 3614; DB 15; Length 715;
Best Local Similarity 98.5%; Pred. No. 1.1e-190;
Matches 673; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
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[illegible]

; AFFILIANI: Rouligne-way, Amelle
 ; TITLE OF INVENTION: Methods and compositions for treating
 ; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395

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Db 334 GSSNQRETGGLSPSTPF-----GASNLLVNPLEPQ 364
QY 531 NADKIRVKIADIGNACWVHKHFTEDIQTRQYSIEVLIGAGYSTPADIWSTACMAFELAT 590
Db 365 NADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGPADIWSTACMAFELAT 424
QY 591 GDLPEPHSGEDYSRDEDEHIAHIELLSIPRHFALSGKYSREFFNRRGELRHITKLPW 650
Db 425 GDLPEPHSGEDYSRDEDEHIAHIELLSIPRHFALSGKYSREFFNRRGELRHITKLPW 484
QY 651 SLFDVLVVKYGWPHEDAAQFTDLIPMLEMVPKESASAGECLRHHPWLN 698
Db 485 GLYEVLMKYEWPLEQATQFSALFLPMMEYIPEKRSASAADCLQHPWLN 532

RESULT 9
US-10-723-860-1549
; Sequence 1549, Application US/10723860
; Publication No. US200404253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 05882.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1549
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-723-860-1549

Query Match 50.3%; Score 1882; DB 17; Length 533;
Best Local Similarity 56.5%; Pred. No. 1.5e-95;
Matches 366; Conservative 62; Mismatches 66; Indels 154; Gaps 7;

QY 52 TP-PEPEEILGSDDEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLWCW 110
Db 38 TPVQMLQGLGSDDEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLWCW 97
QY 111 DMQGRFVAMKVKVSAQHYTETALDEIKLLKCVRESDDSPDKMVMVOLIDDFKISGMNG 170
Db 98 DIQRKRFVAMKVKVSAQHYTETALDEIKLLKCVRESDDSPDKMVMVOLIDDFKISGMNG 157
QY 171 IHVCMVFEVLGHLLKWIILKSNYQGLPVRCKVSIIRQVLQGLDYLHSCCKIHTDIKPEN 230
Db 158 VHVMVFEVLGHLLKWIILKSNYQGLPVRCKVSIIRQVLQGLDYLHSCCKIHTDIKPEN 217
QY 231 ILMCVDDAYVRMAAEATEWQKAGAPPPSGSAVSTAPQKPIGKISKNKKKLLKKQKQR 290
Db 218 ILLCVGDYAIRLAAEAATEWQKAGAPPPSGSAVSTAPQKPIGKISKNKKKLLKKQKQR 277
QY 291 ABLEKRLQIEIELEERAEERKIIENITSAAPNDQDGEYCPVKLKTGTEEAEEAETA 350
Db 278 KRLLEERLRDQLRLE-----AMEAATQAE-- 301
QY 351 KNGGAEPQEEKEDAEKENIEKEDDDVDQELANIDPTWIESPKTNGHTIENGPFSLQQLD 410
Db 302 -DSG----- 304
QY 411 DEDDDEDCPNPEYNLDEPNAESDYTVSSYEQNGELPNGRHKIPESQPEPSTSLFS 470
Db 305 -----LRLDGGSG-----STSSGFGSL-----ESPASCSILS 333
QY 471 GSPLEPVACGSLSEGSPLTEQESSPHDRSRTVSASSTGDLPAKTRAADLLVNPIDPR 530
Db 334 GSSNQRETGGLSPSTPF-----GASNLLVNPLEPQ 364
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QY 531 NADKIRVKIADIGNACWVHKHFTEDIQTRQYSIEVLIGAGYSTPADIWSTACMAFELAT 590
Db 365 NADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEYGPADIWSTACMAFELAT 424
QY 591 GDLPEPHSGEDYSRDEDEHIAHIELLSIPRHFALSGKYSREFFNRRGELRHITKLPW 650
Db 425 GDLPEPHSGEDYSRDEDEHIAHIELLSIPRHFALSGKYSREFFNRRGELRHITKLPW 484
QY 651 SLFDVLVVKYGWPHEDAAQFTDLIPMLEMVPKESASAGECLRHHPWLN 698
Db 485 GLYEVLMKYEWPLEQATQFSALFLPMMEYIPEKRSASAADCLQHPWLN 532

RESULT 10
US-10-369-493-5839
; Sequence 5839, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5839
; LENGTH: 698
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5839

Query Match 36.7%; Score 1374; DB 14; Length 698;
Best Local Similarity 46.4%; Pred. No. 1.8e-67;
Matches 304; Conservative 64; Mismatches 143; Indels 144; Gaps 13;

QY 53 PPEPEEILGSDDEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLWCW 112
Db 96 PMDPGEQ-LGSDDEQEDPRDYKGGYHPVNIQVFNARYHVIRKLGWGHFSTVWLWMDT 154
QY 113 QGKRFVAMKVKVSAQHYTETALDEIKLLKCVRESDDSPDKMVMVOLIDDFKISGMNGIH 172
Db 155 QGKRFVAMKVKVSAQHYTETALDEIKLLKCVRESDDSPDKMVMVOLIDDFKISGMNGIH 214
QY 173 VCMVFEVLGHLLKWIILKSNYQGLPVRCKVSIIRQVLQGLDYLHSCCKIHTDIKPENIL 232
Db 215 VAMVFEVLGCNLLKLIIRSNYRGLHQLQVRKICQVLEALGYMHEKCGIHTDIKPENVL 274
QY 233 MCVDDAYVRMAAEATEWQKAGAPPPSGSAVSTAPQ---QKPIGKISKNKKKLLKKQKQR 289
Db 275 ITMSREEIKIWAQHAVVARKNM-KMGSASVSTAPDHLVKAQENMTKNKKKKKKKKK 333
QY 290 QAELEKRLQIEIELEERAEERKIIENITSAAPNDQDGEYCPVKLKTGTEEAEEAETA 349
Db 334 QREKLEAELAGLEI-----KMDANGLQAYNNAP 363
QY 350 AKDNGEAEDQEE--KEDAEKENIEKEDDDVDQELANIDPTWIESPKTNGHTIENGPFSLQEQ 407
Db 364 ELENFNASQVEDVTMETVNE-----GNRKVEIRSPDFDRITLTFFS--- 408
QY 408 QLDDDDDEDCPNPEY--NLDEPNAESDYTVSSYEQNGELPNGRHKIPESQPFPS 465
Db 409 -----DPESKFGDLASPSAE---YLSS-----PMQQLP--- 433
QY 466 TSLFSGSLPVACGSLSEGSPLTEQESSPHDRSRTVSASSTGDLPAKTRAADLLVN 525
Db 434 ----PGGILPAP----- 441
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QY 526 PLDPNAD---KIRVKIADLGNACWVHKHFTEDIQROYRSEVLIGAGYSTPADIWSTA 582
Db 442 PVPNIGDPYCDLDVKIADLGNACWVHHYTDIIQTRVRALEVLIGSGYPPADIWSTA 501
QY 583 CMAFELATGDLFEPHSGSDYSDRDEHIAHIELLGSIPRHFALSGYKSYREFNRRGELR 642
Db 502 CMAFELATGDLFEPHSGSDYSDRDEHIAHIELLGAIPPSYKKGKHWREFPHKNGHLL 561
QY 643 HITKLPWNSLFDVLVEKYGWPHEDAAQFTDFLIPMLEVPEKASAGCELRHPWL 697
Db 562 HIHQLKPSLYEVLROKYEWSHEDAQQPFESFLRPLDLPQEKXRSTAKIALKHPFL 616

RESULT 11
US-10-369-493-5838
; Sequence 5838, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 5838
; LENGTH: 782
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-5838

Query Match 36.5%; Score 1364.5; DB 14; Length 782;
Best Local Similarity 45.8%; Pred. No. 6.9e-67;
Matches 309; Conservative 75; Mismatches 174; Indels 117; Gaps 16;

QY 53 PPEEEILGSDDEQEDPADYCKGYHPVKIGDLFNGRYHVRKLGWGHFSTVWLCDWM 112
Db 96 PMPDGEQ-LGSDDEQEDPRDKRGYHPVNIQDVFNARYHVRKLGWGHFSTVWLMDT 154
QY 113 QKRFVAMKVSAAHYTETALDEIKLLKCVRESPPDPNKMVYVQLIDDFKISGMNGIH 172
Db 155 QDKRFVAMKIVSAHYTEALDEIKLLSVRSADENDIGCHKVQLLDFEFTVGTNGQH 214
QY 173 VCMVFEVLGHLHLLKWIISKNYOGLPVRCKVSIIRQVGLDYLHSHCKIHTDIKPENIL 232
Db 215 VAMVFEVLGNLLKLIIRSNYRGLHLEQVRKICQVLEALGYMHEKCGIHTDIKPENVL 274
QY 233 MCVDDAYVRMAAEATEWOKAGAPPPSGSAVSTAQ---QKPIGKISXNKKKKLKKQKR 289
Db 275 ITMSREEIKIMAHAVARXNMN-KMSGSAVSTAPDHLVYKMAQENNTKNNKKKKKKRKK 333
QY 290 QALLLEKRLQEIIELEEREAEKRIIEENITSAAPSDQDGEYCEPVKLTGTEEAEEAET 349
Db 334 QREKLEAEALGLEL-----KNDANGLOEA--YNN 361
QY 350 AKDNGEAEQEKEDAEKENIEKDEDDVDQELANIDPTWIESPKTNGHIENGPFSLQQL 409
Db 362 APQNG-----VRMRPSSL-----LFNGP--IPQLL 384
QY 410 D-----DEDDDCPNPEYNLDEPNAESDYTSSSYEQFN---GELPNGRHKIPESOF 461
Db 385 QGSSCVNTSPSPRTVPPPPSLYPQVGCVCNQTYHLTVILNANVGELN----- 434
QY 462 PEFSTSLFGSLPEVACGVLSEGSPLTEQESSPSHDSRTVS-----ASSTGDL--PK 514
Db 435 ---FNAS-----QVEDVTMETVNGNRRNKVRSRDPDRFTLTTPSPDPSKFGDLASPS 488

QY 515 AKTRAAD-----LLVNPDLPRNAD---KIRVKIADLGNACWVHKHFTEDIQROYR 562
Db 489 AYLSSPMSQLPPGGILPAPPVPGNIGDPCYDIDVKIADLGNACWVHHYTDIIQROYR 548
QY 563 STEVLIGAGYSTPADIWSTACMAFELATGDLFEPHSGSDYSDRDEHIAHIELLGSIPR 622
Db 549 ALEVLIGSGYPPADIWSTACMAFELATGDLFEPHSGSDYSDRDEHIAHIELLGAIPP 608
QY 623 HPALSGKYSREFNRRGELRHITKLPWNSLFDVLVEKYGWPHEDAAQFTDFLIPMLEMVP 692
Db 609 STYKKGKHWREFPHKNGHLLHIHQLKPSLYEVLROKYEWSHEDAQQPFESFLRPLDLPDQ 668
QY 683 EKRSAGCELRHPWL 697
Db 669 EKRSATAKIALKHPFL 683

RESULT 12
US-10-425-114-49483
; Sequence 49483, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49483
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700745847_FLI.pep
US-10-425-114-49483

Query Match 28.8%; Score 1076.5; DB 15; Length 550;
Best Local Similarity 39.2%; Pred. No. 3.2e-51;
Matches 255; Conservative 75; Mismatches 120; Indels 201; Gaps 19;

QY 63 SDDEQEDPADYCKGYHPVKIGDLFNGRYHVRKLGWGHFSTVWLCDWMQKRFVAMK 121
Db 21 SEDEGTE---DYRRGGYHVRIGDAPFAGRYVYVQSGKLGWGHFSTVWLMDTKHSRIVALK 77
QY 122 VVKSQAHYTETALDEIKLLKCVRESPPDPNKMVYVQLIDDFKISGMNGIHYCMVFEVLG 181
Db 78 VQKSAHYTEAAMDITILQIAEGDPD--KKCVVLLDHFHKGSPNGHQVCMVFEVLG 135
QY 182 HLLKWIISKNYOGLPVRCKVSIIRQVGLDYLHSHCKIHTDIKPENILM--CVDVAY 239
Db 136 DNLLTLIKYSDVRGLPIAMVKEICFHLIAGLDYLAHQQLSIHTDLKPENILLSTID-- 192
QY 240 VRRMAAEATEWOKAGAP---PPSGS--AVSTAPOQKP---IGKISXNKKKKLKKKQKROA 291
Db 193 -----PSKPRKSGAPLILPNSKDMAMESAGMDTKMLNGDLVKNHKKKIKRKAQAA 246
QY 292 E-LLEKRLQEIIELEEREAEKRIIEENITSAAPSDQDGEYCEPVKLTGTEEAEEAETA 350
Db 247 HCVKEASE-----GVE----- 259
QY 351 KNGBAEQEKEDAEKENIEKDEDDVDQELANIDPTWIESPKTNGHIENGPFSLQQLD 410
Db 260 ---GNAE-----TSGAVES----- 270
QY 411 DEDDDEDCPNPEYNLDEPNAESDYTSSSYEQFNGLPNGRHKIPESQPFESFSLPS 470

Db 271 -----SPNA-----SSAREQ-----TSSSA 285
QY 471 GSLEPVACGVSLS--EGSPLTEQESSPSHDSRTVSASSTGDLPAKAKTRAADLLVNPDLDP 528
Db 286 GT-----SOLSDADGTXLEQGNKGRSRMRQKLLAS-----VDL----- 320
QY 529 PRNADKIRVIADLGNACVWHKHFTEDIOIOTQVRSIEVLIGAGYSTPADIWSTACMAPEL 588
Db 321 -----KCKLVDFGNACWTYKQFTNDIOIOTQVRCPEVILGSKYSTSADLWSFACICPEL 373
QY 589 ATGDVLFPHSGEDYSRDEDHIAHIIELGSGIPRHFALSGKYSREFFNRGELRHITKX 648
Db 374 ATGDVLFPHSGDNDRDEHDLALMELLGMPRKIALGGYRSRDFNRYGDLRHIRLR 433
QY 649 PWSLFDVLEKYGWPHEDAAQFTDFLIPMLEVMPEKRSAGECLRHPLWNS 699
Db 434 FWPLNKVLEKYLSEKDANDMTDFLVPILDFVPEKRPTAGCQLLHPWNA 484

RESULT 13
US-10-424-599-215731
; Sequence 215731, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215731
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36833C.1.pep
US-10-424-599-215731

Query Match 28.6%; Score 1071.5; DB 15; Length 547;
Best Local Similarity 38.5%; Pred. No. 6.1e-51;
Matches 250; Conservative 76; Mismatches 126; Indels 197; Gaps 17;
QY 63 SDEQEDPADYCKGYHPVKIGDLF--GRYHVIRKLGWGHFSTVWLCWDMQGRFVAMK 121
Db 18 SEDEGTE---DYRRGGYHVRIGDAFSAGRYVVOQSLGWHGFSTVWLAWDTKHSRYVALK 74
QY 122 VVKSQAQHYTETALDEIKLLKCVRESPPSDPNKDMVVQLIDDFKISGMNGIHYCMVFEVLG 181
Db 75 VQKSAQHYTEAAMDEITILQIAEGDPD--KKCVVKLLDHFHKGSPNGQHVCMVFEVLG 132
QY 182 HLLKWIITKSNYQGLPVRCKSIIRQVLOGLDYLSKCKIIHTDIKPENILM--CVDDAY 239
Db 133 DNLLTLIKYSDYRGVPLHVMVKEICFHILVGLDYLHRELSIHTDIKPENILLSTID--- 189
QY 240 VERMAAEATEWOKAGAP---PPSGS--AVSTAPQKP---IGKSNKKKKLKKKQKQA 291
Db 190 -----PSKDKRSGAPLILPNSKQKMAWESGMDKDTMLNGDLVKNHKKIKRKAQQA 243
QY 292 E-LLEKRLQIELEEREAEERKIIIEENITSAFNSDQDGEYCPVKLKTGTEAAEAETA 350
Db 244 HCVKEKEASE-----GVE----- 256
QY 351 KONGEADEQEKEDAENIEKDEDDVDQELANIDPTWIESPKTNCHIENGPFSLQQLD 410
Db 257 ---GNAE-----TSGAVES----- 267
QY 411 DEDDDEEDCPPEYNLDEPNAESDYTSYSSVEQFNGELPNGRHKIPESQPFESTSLFS 470
Db 268 -----SPNASSAREQASS-----SAGTSRLS 288

QY 471 GSLEPVACGVSLSSEGSPLTEQESSPSHDSRTVSASSTGDLPAKAKTRAADLLVNPDLDP 530
Db 289 D-----ADGTXLEQGNKGRSRMRQKLLA-----LVD----- 316
QY 531 NADKIRVIADLGNACVWHKHFTEDIOIOTQVRSIEVLIGAGYSTPADIWSTACMAPEL 590
Db 317 -----LKCKLVDFGNACWTYKQFTNDIOIOTQVRCPEVILGSKYSTSADLWSFACICPEL 372
QY 591 GDYLFEPHSGEDYSRDEDHIAHIIELGSGIPRHFALSGKYSREFFNRGELRHITKX 650
Db 373 GDVLFPHSGDNDRDEHDLALMELLGMPRKIALGGYRSRDFNRYGDLRHIRLR 432
QY 651 SLFDVLEKYGWPHEDAAQFTDFLIPMLEVMPEKRSAGECLRHPLWNS 699
Db 433 PLNKVLEKYLSEKDANDMTDFLVPILDFVPEKRPTAGCQLLHPWNA 481
RESULT 14
US-10-739-930-5613
; Sequence 5613, Application US/10739930
; Publication No. US20040216190A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 5613
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: ABATH-23APR03-C1089_1.p
US-10-739-930-5613

Query Match 28.5%; Score 1067; DB 17; Length 538;
Best Local Similarity 37.2%; Pred. No. 1.1e-50;
Matches 242; Conservative 81; Mismatches 117; Indels 210; Gaps 16;
QY 63 SDEQEDPADYCKGYHPVKIGDLF--GRYHVIRKLGWGHFSTVWLCWDMQGRFVAMK 121
Db 18 SEDEGTE---DYRRGGYHVRIGDAFSAGRYVVOQSLGWHGFSTVWLAWDTKHSRYVALK 74
QY 122 VVKSQAQHYTETALDEIKLLKCVRESPPSDPNKDMVVQLIDDFKISGMNGIHYCMVFEVLG 181
Db 75 IQKSAQHYTEAAMDEIKLQIAEGDAED--KKCVVKLLDHFHKGSPNGQHVCMVFEVLG 132
QY 182 HLLKWIITKSNYQGLPVRCKSIIRQVLOGLDYLSKCKIIHTDIKPENILM--VDDAY 239
Db 133 DNLLSVIKYSDYRGVPLHVMVKEICFHILVGLDYLHRELSIHTDIKPENILLSTIDP-- 190
QY 240 VERMAAEATEWOKAGAPPPSGSAVSTAPQKPIGK-----IGKSNKKKKLKKKQK 288
Db 191 -----EADA--RKSGIPVLPTVKDQKAVPERPVEKEPKSYTSADLTNKKKIRKK-- 241
QY 289 ROAELLEKRLQIELEEREAEERKIIIEENITSAFNSDQDGEYCPVKLKTGTEAAEA 348
Db 242 -----AKVSGSENERDS-----SNS- 259
QY 349 TAKONGEADEQEKEDAENIEKDEDDVDQELANIDPTWIESPKTNCHIENGPFSLQQLD 408
Db 260 -ARPNGNATVERLBESSER---VKDAENVSO-----KSRGN----- 291
QY 409 LDEDDDEEDCPPEYNLDEPNAESDYTSYSSVEQFNGELPNGRHKIPESQPFESTSL 468
Db 292 -----TSGAVES----- 291
QY 469 FSGSLEPVACGVSLSSEGSPLTEQESSPSHDSRTVSASSTGDLPAKAKTRAADLLVNPDL 528
Db 292 -----RRGSRSTRQK-----LLA----- 304

Qy	529	PRNADKIRVKIADIGNACWVHHGFTTDTOTQYRSIEVLIGAGYSTPADIMSTACWAFEL	588
		: :	
Db	305	--DVDR--KCKLVDFGNACWTYKQFTSDITQRYRCPEVVLSGYSKYSTADMWSFACICEP	361
		: :	
Qy	589	ATGDYLPEPHSGEDYSRDEDHAIHIELLSIPRHFAISGKYSRREFNRGRBELRHITHUK	648
		: :	
Db	362	ATGDVLFDPPHSGENFERDEDHLAMMELLGMWPRIALGRRHSRDOFFNRQGSELHRRLR	421
		: :	
Qy	649	PWSLFDFVLVEKYGHPHEDAAQFTDPLI PMLEVMVPKRASAGECLRHPIWLIN	698
		: :	
Db	422	FWPLSKVLTKDYKSEEDAIAMQDPITFILOFVPEKRTTAOQLTHPWLN	471
		: :	

RESULT 15

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RES001.13
US-10-369-493-12951
; Sequence 12951, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xinfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEIN
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12951
; LENGTH: 561
; TYPE: PRP
; ORGANISM: Aspergillus nidulans
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(561)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12951

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Query Match	28.2%;	Score 1054;	DB 14;	Length 561;
Best Local Similarity	37.6%;	Pred. No. 5.7e-50;		
Matches 247;	Conservative 85;	Mismatches 161;	Indels 164;	Gaps 13;
Qy	57	EEETISDDDEOEADPYCKGGYHPVKIGDLF-NGRYHVIRKLGWGHFSTVWLCDWQGX	115	
Db	23	EEEE--ETTAEEEDSEDYCKGGYHPVQIGELYNNGRVYVVRKLGWGHFSTVWLSRDTTG	80	
Qy	116	RFVAMKVVKGAQHYTETALDEIKLLKCVRESDDPNKMDWVYQI:IDPFKISGMNGIHCVM	175	
Db	81	KHVALKVVRSAAHYTETAIDEIKLLNRIVQANSPHGRKHVVSVLLDSFEHKGPRGHVCM	140	
Qy	176	VFEVLGHLLKWIITKSNVQGLPVCVKSIITROVLGLDYLHSCKIITHDTIKPNI:MCV	235	
Db	141	VFEVLGENLGLI:KKNWHRGIMP:LVQITKQVLGLDYLHRECGI:IIHTDUKPENLIEI	200	
Qy	236	DDAYVRMAAEATEWQKAGAPPPSGSVAVTAPOQKPIKIS:KNKKKLLKKQKQAEILLE	295	
Db	201	GDV-----EQIVKTVYVKEAKKEQEDNNG-----	226	
Qy	296	KRLQIEELREARPKI:IEENITSAAPSNODGECYCEVKUKTTGLGLEAAEAETAKONGE	355	
Db	227	-----RRRRRTLITGSQPLPSP-----LNTT-----PEFKHSSONSH	258	
Qy	356	AEDQEEKEDAEKENIEKDEDDVDVQELANIDPTWIESPKTNGHIENGPPSLEQQQLDDEDD	415	
Db	259	SSLSQVINESPGXNFQISENXT-----MLIGTGTSEAP-----SMRQLIGIKDED	303	
Qy	416	EEDCPNEPNYLDPEPNAESDYTVSSSYEQFNGLPNGRHKIPESQPFPEFSTSLFSGSLEP	475	
Db	304	EOO-----KOREK-----TAYVER	317	

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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	3742	100.0	699	4	US-09-759-359A-2	Sequence 2, Appli	
2	3742	100.0	699	4	US-10-207-973-2	Sequence 2, Appli	
3	3620	96.7	688	2	US-09-016-000-2	Sequence 2, Appli	
4	2070.5	55.3	655	1	US-08-264-002-2	Sequence 2, Appli	
5	1374	36.7	1087	1	US-08-364-002-5	Sequence 5, Appli	
6	979.5	26.2	544	1	US-08-364-002-7	Sequence 7, Appli	
7	979.5	26.2	544	3	US-09-457-040B-15	Sequence 15, Appli	
8	835	22.3	297	3	US-09-173-581-1	Sequence 1, Appli	
9	835	22.3	297	3	US-09-420-915-1	Sequence 1, Appli	
10	746.5	19.9	576	4	US-09-248-796A-20509	Sequence 20509, A	
11	363	9.7	112	4	US-09-670-767-32637	Sequence 32637, A	
12	363	9.7	112	4	US-09-270-767-47854	Sequence 47854, A	
13	340.5	9.1	499	3	US-09-457-040B-13	Sequence 13, Appli	
14	334.5	8.9	499	4	US-09-905-999-21	Sequence 21, Appli	
15	321.5	8.6	490	4	US-09-376-594-314	Sequence 314, Appli	
16	321.5	8.6	490	4	US-09-905-999-23	Sequence 23, Appli	
17	318	8.5	568	4	US-08-835-170-4	Sequence 4, Appli	
18	318	8.5	568	3	US-09-359-257-4	Sequence 4, Appli	
19	318	8.5	588	2	US-08-835-170-2	Sequence 2, Appli	
20	318	8.5	588	3	US-09-359-257-2	Sequence 2, Appli	
21	317.5	8.5	429	4	US-09-810-671-5	Sequence 5, Appli	
22	317.5	8.5	429	4	US-10-109-854-5	Sequence 5, Appli	
23	317.5	8.5	429	4	US-10-339-656-5	Sequence 5, Appli	
24	317.5	8.5	484	3	US-09-457-040B-12	Sequence 12, Appli	
25	316	8.4	568	3	US-09-371-674-4	Sequence 4, Appli	
26	316	8.4	598	3	US-09-371-674-2	Sequence 2, Appli	
27	313.5	8.4	517	3	US-09-457-040B-14	Sequence 14, Appli	

Db 361 EKDAEKENIEKDDDDVQDELANIPTWIESPKTNGHIENGPFSLFQQLDDDDDEEDCP 420
QY 421 NPEEYNLDEPNAESDYTYSSSYEQFNGELPNGRHKIPESQPFSTSLFSGSLEPVACGS 480
Db 421 NPEEYNLDEPNAESDYTYSSSYEQFNGELPNGRHKIPESQPFSTSLFSGSLEPVACGS 480
QY 481 VLSEGSPLTEQESSPSHDRSRTVSASSTGDLPAKTRAADLLVNLDPNADKIRVKIA 540
Db 481 VLSEGSPLTEQESSPSHDRSRTVSASSTGDLPAKTRAADLLVNLDPNADKIRVKIA 540
QY 541 DLGNACWVHKHFTEDIOTROYRSIEVLICAGYSTPADIWSTACMAFELATGDYLFEPHSG 600
Db 541 DLGNACWVHKHFTEDIOTROYRSIEVLICAGYSTPADIWSTACMAFELATGDYLFEPHSG 600
QY 601 EDYSRDEDHIAHIELLGSIPRHFALSGKYSREFNRRGELRHITKLPWSLFDVLVEKY 660
Db 601 EDYSRDEDHIAHIELLGSIPRHFALSGKYSREFNRRGELRHITKLPWSLFDVLVEKY 660
QY 661 GWPHEHAAQFTDFLIPMLEMVEPKRASAGECLRHPLWLS 699
Db 661 GWPHEHAAQFTDFLIPMLEMVEPKRASAGECLRHPLWLS 699

RESULT 2
US-10-207-973-2
; Sequence 2, Application US/10207973
; Patent No. 6753175
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROEF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/10/207,973
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Human
US-10-207-973-2

Query Match. 100.0%; Score 3742; DB 4; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.7e-251;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSRKVLAIQARKRPKREKHPKPEPOQKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPPPEEI 60
Db 1 MSSRKVLAIQARKRPKREKHPKPEPOQKAPLVPPPPPPPPPPPPPPPPPPPPPPPPPPPEEI 60
QY 61 LGSDDDEEDPADYCKGGVHPVKIGDLFNGRVHVRKLGWGHFSTVWLCWDMQGRFVAM 120
Db 61 LGSDDDEEDPADYCKGGVHPVKIGDLFNGRVHVRKLGWGHFSTVWLCWDMQGRFVAM 120
QY 121 KVKSQAHYTETALDEIKLLKCVRESDFSPNKMVQVLIIDFKISGNHGHVCMVFEVL 180
Db 121 KVKSQAHYTETALDEIKLLKCVRESDFSPNKMVQVLIIDFKISGNHGHVCMVFEVL 180
QY 181 GHLLKWLKSNYQGLPVRCKSIIRQVLQGLDYLHSCKIIHTDIKENTILMVCVDDAYV 240
Db 181 GHLLKWLKSNYQGLPVRCKSIIRQVLQGLDYLHSCKIIHTDIKENTILMVCVDDAYV 240
QY 241 RMAAEATEWQAGAPPPSGSVAVTAPOQKPIGKTSKNNKKLKKKQKQAELEKRLQE 300
Db 241 RMAAEATEWQAGAPPPSGSVAVTAPOQKPIGKTSKNNKKLKKKQKQAELEKRLQE 300
QY 301 IEELEREARKIIENITSAFNSDQDGEYCEPVKLTGTGLEAAAEATAKONGAEADQE 360
Db 301 IEELEREARKIIENITSAFNSDQDGEYCEPVKLTGTGLEAAAEATAKONGAEADQE 360
QY 361 EKDAEKENIEKDDDDVQDELANIPTWIESPKTNGHIENGPFSLFQQLDDDDDEEDCP 420

Db 361 EKDAEKENIEKDDDDVQDELANIPTWIESPKTNGHIENGPFSLFQQLDDDDDEEDCP 420
QY 421 NPEEYNLDEPNAESDYTYSSSYEQFNGELPNGRHKIPESQPFSTSLFSGSLEPVACGS 480
Db 421 NPEEYNLDEPNAESDYTYSSSYEQFNGELPNGRHKIPESQPFSTSLFSGSLEPVACGS 480
QY 481 VLSEGSPLTEQESSPSHDRSRTVSASSTGDLPAKTRAADLLVNLDPNADKIRVKIA 540
Db 481 VLSEGSPLTEQESSPSHDRSRTVSASSTGDLPAKTRAADLLVNLDPNADKIRVKIA 540
QY 541 DLGNACWVHKHFTEDIOTROYRSIEVLICAGYSTPADIWSTACMAFELATGDYLFEPHSG 600
Db 541 DLGNACWVHKHFTEDIOTROYRSIEVLICAGYSTPADIWSTACMAFELATGDYLFEPHSG 600
QY 601 EDYSRDEDHIAHIELLGSIPRHFALSGKYSREFNRRGELRHITKLPWSLFDVLVEKY 660
Db 601 EDYSRDEDHIAHIELLGSIPRHFALSGKYSREFNRRGELRHITKLPWSLFDVLVEKY 660
QY 661 GWPHEHAAQFTDFLIPMLEMVEPKRASAGECLRHPLWLS 699
Db 661 GWPHEHAAQFTDFLIPMLEMVEPKRASAGECLRHPLWLS 699

RESULT 3
US-09-016-000-2
; Sequence 2, Application US/09016000
; Patent No. 5962232
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; TITLE OF INVENTION: PROTEIN KINASE MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,000
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0465 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HEARNOT01
; CLONE: 307624


```
RESULT 5
US-08-264-002-5
; Sequence 5, Application US/08264002
; Patent No. 5559019
; GENERAL INFORMATION:
; APPLICANT: GUI, JIAN-FANG
; APPLICANT: FU, XIANG-DONG
; TITLE OF INVENTION: NOVEL PROTEIN SERINE KINASE, SRPK1
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 Century Park East, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,002
; FILING DATE: 22-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN PH.D., LISA A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD3590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1087 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; CLONE: CEHK
; NAME/KEY: Protein
; LOCATION: 1..1087
US-08-264-002-5

Query Match 36.7%; Score 1374; DB 1; Length 1087;
Best Local Similarity 46.7%; Pred. No. 5.6e-87;
Matches 305; Conservative 68; Mismatches 158; Indels 122; Gaps 13;

QY 53 PPEEEILGSDDEQEDPADYCKGGYHPVKIGDLFNGRYHYVIRKLGWGHSTVWLCDWM 112
DB 481 PMPDGEQ-LGSDDEQEDPRDYKGGYHPVNGDVFNARYHVIRKLGWGHSTVWLAWDT 539
QY 113 QGKRVAMKVKSAGHYETALDEIKLKCVRSDPSDPNKMVYQLIDDFKISGMNGIH 172
DB 540 QDKRVAMKIVKSAHYETAALDEIKLLSVRSADPNIGCHVKVQLDFEFTVINGQH 599
QY 173 VCMVEVILGHLLKWKIISNVQGLPVRVCVKSIIROVLQGLDYLHSCVKIITHDKPENIL 232
DB 600 VAMVPEVLGNLLKLIIRSNVRLGLEQVRKICQVLEALGYMHEKCGIITHDKPENVL 659
QY 233 MCVDDAYVRRMAAEATEQKAGAPPPSGSAVSTAQ---QKPIGKISNKKKLLKKQKR 289
DB 660 IIMSREEIKIMQAHAVARKMM-KVSGSAVSTAQPHLVKMAQENWTKNKKKKKKKAKK 718
QY 290 QAELEKRLQETEELEBAERKIIIEENITSAAPSNDQGEYCEPVKLKTTTGLEAAEAET 349
DB 719 QREKLEAELAGLEGLKMDANG--LQEAYNAPLTNIGKVMCNRRNGTLEENF----- 771
QY 350 AKDNGEAEDEQEKEDAENIEKEDDDVDQELANIDPTWIESPKTNNGHIENGPFSLQOL 409

Db 772 ---NASQVEDVTMEDTVNEN-----GNRNKVEIRSPDRFDRFTLTTPFS----- 811
QY 410 DDEDDDEDCNPBEY--NLDEPNAESDYTYSSSYEQFNGELPNGRHKIPESQFPEFSFS 467
DB 812 -----DPESKFGDLASPSAE---YLSS-----PMSQLP----- 836
QY 468 LFGSLPEFVACGVLSEGSPLTEQESFSHDSRTVSASSTGDLPKAKTRAADLLVNPL 527
DB 837 --PGGILPAP-----PV 846
QY 528 DPNRAD---KIRVKIADLGNACWVHKHFTEDIQTRYRSIEVLIGAGYSTPADINWSTACM 584
DB 847 GFNIGDPYCDIDVKIADLGNACWVNNHYTDDIQTRYRALEVLIGSGYGPADINWSTACM 906
QY 585 AFELATGDLPEPHSGEDYSRDEDDHIAHIELGSIPIRHFAISGKYSREFFNRRGELRHI 644
DB 907 AFELATGDLPEPHSGEDYSRDEDDHLAHSSELLGAIPFSIYKKGKHWREFFHKNGHLLHI 966
QY 645 TKLKPWSLFDVLVEKYGWPHEDAAQFTDPLPMLMPEKVASAGECLRHHPWL 697
DB 967 HQLKPWSLYEVLROKYEWSHEDAQQFESFLRPLDQFQEKSTAKIALKHPFL 1019

RESULT 6
US-08-264-002-7
; Sequence 7, Application US/08264002
; Patent No. 5559019
; GENERAL INFORMATION:
; APPLICANT: GUI, JIAN-FANG
; APPLICANT: FU, XIANG-DONG
; TITLE OF INVENTION: NOVEL PROTEIN SERINE KINASE, SRPK1
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 Century Park East, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,002
; FILING DATE: 22-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN PH.D., LISA A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD3590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-264-002-7

Query Match 26.2%; Score 979.5; DB 1; Length 544;
Best Local Similarity 36.6%; Pred. No. 5.5e-60;
Matches 233; Conservative 68; Mismatches 154; Indels 181; Gaps 12;

QY 68 QEDPADYCKGGYHPVKIGDLFNGRYHYVIRKLGWGHSTVWLCDWMQKGRFVAMKVKS 126
DB 56 EENAEDHYGGYHPVYIGEEFHRRYVVERKLGWGHSTVWLAYDRAAKRRVALKVRSA 115
QY 127 QHYETALDEIKLKCVRSDPSDPNKMVYQLIDDFKISGMNGIHVCMVEVLGHLLK 186
```

Db 116 EHYRETSIDEIRLOKIREGDEKHLGKHHIISLLDYFVHRGPNGAHVCVFEVLGENLLS 175
Qy 187 WIKSNYQGLPVRCKSIIRVOQLDYLHSHCKIIHTDIPENILMVCVDDAYVRRMAAE 246
Db 176 LIQSYGHRGVPVGIKQIAYQLLIALDYLHRECGIHTDLKPENVLICIDQALQHEAP 235
Qy 247 ATEWOKAGAPPSPGSAVSTAPQOKPIGKISKNKKLKKQKQABLLKRLQEIIEELER 306
Db 236 ATT-----SSPTNTSSS-----KTRNTGYTAKAPII-KRGQSVNNSAQ 274
Qy 307 EAERKIIIBENITSAAPNSDQDGEYCEPVKLKTT-----GLEBAEAEATAKNGEADQEE 361
Db 275 --ERKTFAPKNPTK---NSKPAGQVIPSPTSTLSRFPSPLEGAVSISLRD----- 320
Qy 362 KEDAENIEKEDDDVDQELANIDPTWIESPTKNGHIENGSPFSLEQQLDDEDDDEDCPN 421
Db 321 ----SOKHNSH-PNSPFS----- 335
Qy 422 PBEYNLDEPNAESDYTYSSSYEQFNGELPNGRHKIPESQFPPEFSTLSFGSLEPVACGSV 481
Db 336 DNSLILDGVN-----GSOEPV----- 351
Qy 482 LSEGSPLTEQBESSPHDRSRTVSASSTGDLPAKTRAADLLVNPDPNADKIRVKIAD 541
Db 352 -----PKITVKIAD 360
Qy 542 LGNACWVHKHFTEDIQTRYRSIEVLIGAGYSTPADINWSTACWAFELATGDLFEPHSGE 601
Db 361 LGNACWTRKHFTNDVQTRYRSPEVILGCRWGSADCSFACIIFELLTGDLVDFPRNGN 420
Qy 602 DYSRDEDHIAHIELLGSIPRHFALSGKYSRREFFNRGELRHITKLPKSLDFVLVEKYG 661
Db 421 SYSKEDDHIAQIIELLVNYPKQWALSGKHSRDLFNRGELRNHKLKFWPLKDVLEQKYH 480
Qy 662 WPHEDAAQFTDLIPMLEVMVPEKASAGECLRHPL 697
Db 481 FSAELAQAQISDFLSPMLCFDPKAKTNAGYMSNPWL 516

RESULT 7

US-09-457-040B-15
; Sequence 15, Application US/09457040B
; Patent No. 6387641
; GENERAL INFORMATION:
; APPLICANT: Vertex Pharmaceuticals Incorporated
; APPLICANT: Bellon, Steve
; TITLE OF INVENTION: Crystallized p38 Complexes
; FILE REFERENCE: VPI/98-14
; CURRENT APPLICATION NUMBER: US/09/457,040B
; CURRENT FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Human
US-09-457-040B-15

Query Match 26.2%; Score 979.5; DB 3; Length 544;
Best Local Similarity 36.6%; Pred. No. 5.5e-60;
Matches 233; Conservative 68; Mismatches 154; Indels 181; Gaps 12;

Qy 68 QBDPADYKGGYHPVKIGDLFNGRYHVI-RKLGWGHFSTWLCWQGRFVAMKVKVSA 126
Db 56 EENAEDYHGGYHPVYIGEFHRRYVVERKLGWGHFSTWLCWQGRFVAMKVKVSA 115
Qy 127 QHYETALDEIKLKCVRSDSDPNKMVQLIDDFKISGNGHIVCMVFEVLGHLLK 186
Db 116 EHYRETSIDEIRLOKIREGDEKHLGKHHIISLLDYFVHRGPNGAHVCVFEVLGENLLS 175
Qy 187 WIKSNYQGLPVRCKSIIRVOQLDYLHSHCKIIHTDIPENILMVCVDDAYVRRMAAE 246

Db 176 LIQSYGHRGVPVGIKQIAYQLLIALDYLHRECGIHTDLKPENVLICIDQALQHEAP 235
Qy 247 ATEWOKAGAPPSPGSAVSTAPQOKPIGKISKNKKLKKQKQABLLKRLQEIIEELER 306
Db 236 ATT-----SSPTNTSSS-----KTRNTGYTAKAPII-KRGQSVNNSAQ 274
Qy 307 EAERKIIIBENITSAAPNSDQDGEYCEPVKLKTT-----GLEBAEAEATAKNGEADQEE 361
Db 275 --ERKTFAPKNPTK---NSKPAGQVIPSPTSTLSRFPSPLEGAVSISLRD----- 320
Qy 362 KEDAENIEKEDDDVDQELANIDPTWIESPTKNGHIENGSPFSLEQQLDDEDDDEDCPN 421
Db 321 ----SOKHNSH-PNSPFS----- 335
Qy 422 PBEYNLDEPNAESDYTYSSSYEQFNGELPNGRHKIPESQFPPEFSTLSFGSLEPVACGSV 481
Db 336 DNSLILDGVN-----GSOEPV----- 351
Qy 482 LSEGSPLTEQBESSPHDRSRTVSASSTGDLPAKTRAADLLVNPDPNADKIRVKIAD 541
Db 352 -----PKITVKIAD 360
Qy 542 LGNACWVHKHFTEDIQTRYRSIEVLIGAGYSTPADINWSTACWAFELATGDLFEPHSGE 601
Db 361 LGNACWTRKHFTNDVQTRYRSPEVILGCRWGSADCSFACIIFELLTGDLVDFPRNGN 420
Qy 602 DYSRDEDHIAHIELLGSIPRHFALSGKYSRREFFNRGELRHITKLPKSLDFVLVEKYG 661
Db 421 SYSKEDDHIAQIIELLVNYPKQWALSGKHSRDLFNRGELRNHKLKFWPLKDVLEQKYH 480
Qy 662 WPHEDAAQFTDLIPMLEVMVPEKASAGECLRHPL 697
Db 481 FSAELAQAQISDFLSPMLCFDPKAKTNAGYMSNPWL 516

RESULT 8

US-09-173-581-1
; Sequence 1, Application US/09173581A
; Patent No. 6013455
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/173,581A
; CURRENT FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 119819
US-09-173-581-1

Query Match 22.3%; Score 835; DB 3; Length 297;
Best Local Similarity 45.1%; Pred. No. 2.7e-50;
Matches 188; Conservative 32; Mismatches 73; Indels 124; Gaps 10;
Qy 283 LKKQKQKQAELEKRLQEIIEELERAEARKIIBENITSAAPNSDQGEYCEPVKLKTTGLE 342
Db 1 MRKQKQKRLIEERLRLQL----- 22
Qy 343 EAAEAEATAKNGEADQEEKEKDAENIEKEDDDVDQELANIDPTWIESPTKNGHIENG 402

Db 23 EAMEAAT-----QAEDSGLRLDGGSGTSSGCHP-----GGARAGP 59
Qy 403 FSLEQQLDDEDDDCNPEYNLDPENAESDYTYSSSYEQFNGELPNGRHKIPESQFP 462
Db 60 -----SPASSPAP-----CGGRSLSGSQTs 81
Qy 463 EFTSLFSGSLPEPVACGVLSEGSPLTQEESPSHDSRTVSASSTGDL--PKAKTRAA 520
Db 82 GFSGSLFS---PASC-SILSGSS---NQRE-----TGGLLSPSPFFGAS 118
Qy 521 DLLVNPDPNADKIRVKIADLGNACWVHKHFTEDIQTRQYRSIEVLIGAGYSTPADTWS 580
Db 119 NLLVNPDPQADKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAGYSTPADTWS 178
Qy 581 TACMAFELATGDLPEPHSGEDYSRDEDHIAHIELLGSIPRHPFALSGKYSREFFNRGE 640
Db 179 TACMAFELATGDLPEPHSGEDYSRDEDHIAHIELLGSIPRHPFALSGKYSREFFNRGE 238
Qy 641 LRHITKLPMSLFDVLVEKYGWPHEDAAQFTDFLIPMLEMVPKRSAGECLRHFWL 697
Db 239 LRHIHNLKHWGLYEVLMEKYEWPLEQATQFSAFLLPMNEYIPEKRSARDCLQHPWL 295

RESULT 9

US-09-420-915-1

; Sequence 1, Application US/09420915

; Patent No. 6264947

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Tang, Y. Tom

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Yue, Henry

; APPLICANT: Guegler, Karl J.

; APPLICANT: Corley, Neil C.

; APPLICANT: Gorgone, Gina

; APPLICANT: Azimzai, Yalda

; APPLICANT: Lu, Aina

; TITLE OF INVENTION: Protein Kinase Homologs

; FILE REFERENCE: PF-0614 US

; CURRENT APPLICATION NUMBER: US/09/420,915

; CURRENT FILING DATE: 1999-10-20

; EARLIER FILING DATE: 1999-10-20

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PERL Program

; SEQ ID NO 1

; LENGTH: 297

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: -

; OTHER INFORMATION: 119819

US-09-420-915-1

Query Match 22.3%; Score 835; DB 3; Length 297;
Best Local Similarity 45.1%; Pred. No. 2.7e-50;
Matches 188; Conservative 32; Mismatches 73; Indels 124; Gaps 10;

Qy 283 LKKKQKQAELEKRLQETEELEERAEARKIIEENITSAPSDQDGEYCPEVKLTGTLG 342
Db 1 MRKKQKRLLEERLDRQL----- 22
Qy 343 EAAAEATKDNGEAEQDEKEDEDAEKENIEKEDVDQELANIDPTWIESPKTNHENG 402
Db 23 EAMEAAT-----QAEDSGLRLDGGSGTSSGCHP-----GGARAGP 59
Qy 403 FSLEQQLDDEDDDCNPEYNLDPENAESDYTYSSSYEQFNGELPNGRHKIPESQFP 462
Db 60 -----SPASSPAP-----CGGRSLSGSQTs 81
Qy 463 EFTSLFSGSLPEPVACGVLSEGSPLTQEESPSHDSRTVSASSTGDL--PKAKTRAA 520
Db 82 GFSGSLFS---PASC-SILSGSS---NQRE-----TGGLLSPSPFFGAS 118

Qy 521 DLLVNPDPNADKIRVKIADLGNACWVHKHFTEDIQTRQYRSIEVLIGAGYSTPADTWS 580
Db 119 NLLVNPDPQADKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAGYSTPADTWS 178
Qy 581 TACMAFELATGDLPEPHSGEDYSRDEDHIAHIELLGSIPRHPFALSGKYSREFFNRGE 640
Db 179 TACMAFELATGDLPEPHSGEDYSRDEDHIAHIELLGSIPRHPFALSGKYSREFFNRGE 238
Qy 641 LRHITKLPMSLFDVLVEKYGWPHEDAAQFTDFLIPMLEMVPKRSAGECLRHFWL 697
Db 239 LRHIHNLKHWGLYEVLMEKYEWPLEQATQFSAFLLPMNEYIPEKRSARDCLQHPWL 295

RESULT 10

US-09-248-796A-20509

; Sequence 20509, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 20509

; LENGTH: 576

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-20509

Query Match 19.9%; Score 746.5; DB 4; Length 576;
Best Local Similarity 31.3%; Pred. No. 8.6e-44;
Matches 188; Conservative 83; Mismatches 174; Indels 155; Gaps 13;

Qy 143 VRESDDSPDKDMVMVQLIDDFKISGMNGIHVCMVFEVLGHLLKWKIISNQGFLPVRCK 202
Db 4 VTTSDIHHPGHQHVQLDFTTHKGPNGVHVVMVFEVLGENLLGLIRYKRGIPVVFVK 63
Qy 203 SIIRQVQLGDLVHLSKCKIHTDIKPENILCMVDVAYVRRMAAEATEWQKAGAPPSGA 262
Db 64 QIAKQLLSALDFLRQCGVIHTDLKPENILIEIGD----- 98
Qy 263 VSTAPQKPIGKISKNKKKLKKQKQAELEKRLQETEELEERAEARKIIEENITSAP 322
Db 99 -----VEQIVKLVEE-ENLQKQLKRLSRTASKTSTP 129
Qy 323 -SNDQDGEYCPEVKLTGTLGEEAAEATAKDN-----GEAE 357
Db 130 ISATPNSFSNHNANTTTTTTTAKKISINDSIISPTSSALTSSNFHNSPLSGRSG 189
Qy 358 DQEEKED--AKENIEKEDDDVDQELANI---DPTWIESPKTNHENGPPS----- 404
Db 190 RRTRETTLLITGSQPLSPRLSRFNKSFNTVYGLSSSTTNPVRNISINSNNFSSFINNSNT 249
Qy 405 -----LEQQLDDEDDDCNPEYNLDPENAESDYTYSSSYEQFNGELPNGRHKIP 457
Db 250 ANTTNGTATTTEDEEDGE-----NOTLNLSNMSITNSHN----- 288
Qy 458 ESQPEFSTSLFSGSLPEPVACGVLSEGSPLTQEESPSHDSRTVSASSTGDLPKAKT 517
Db 289 -----SNSYQPTATNV---DPVQIPQESVSLDSS---SANVVED----- 323
Qy 518 RAADLLVNPDPNADKIRVKIADLGNACWVHKHFTEDIQTRQYRSIEVLIGAGYSTPAD 577
Db 324 -----IIN-----DNEISVKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAGY 373
Qy 578 TWSTACMAFELATGDLPEPHSGEDYSRDEDHIAHIELLGSIPRHPFALSGKYSREFFNR 637

Db 374 LWSFACLIPELLTGDLPPDRGSKYKDDDDHIAQIIELIGPFPNQMLKESYYAREFFNS 433
QY 638 RCELHRIKLPKWSLFDVLVEKYGPHEDAAQFTFLIPMLEWPEKRSASAGECLRHFWL 697
Db 434 RYELRRIMKLPWGLQDLVLEIKYKFLPNDIAIBSEFLLEMLKLPKEERADAGGMLNHPWL 493

RESULT 11

US-09-270-767-32637
; Sequence 32637, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32637
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-32637

Query Match 9.7%; Score 363; DB 4; Length 112;
Best Local Similarity 54.7%; Pred. No. 4.3e-18;
Matches 70; Conservative 18; Mismatches 18; Indels 22; Gaps 2;
QY 488 LTEQESSPSHRSRTVSASSTGDLPAKAKTRAADLLVNPDPNADKIRVKIADLGNACW 547
Db 7 IPSQSQSSQNTYTIQS-----LIDN-----SNVRVKIADLGNACY 44
QY 548 VHKHFTEDIQTRQYSIEVLIGAGYSTPADINSTACMAFELATGDLPEPHSGEDYSRDE 607
Db 45 DVHHTFEDIQTRQYSIEVLIGAGYSTPADINSTACMAFELATGDLPEPHSGEDYSRDE 104
QY 608 DHIAHIE 615
Db 105 DHLAHIVD 112

RESULT 12

US-09-270-767-47854
; Sequence 47854, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47854
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-47854

Query Match 9.7%; Score 363; DB 4; Length 112;
Best Local Similarity 54.7%; Pred. No. 4.3e-18;
Matches 70; Conservative 18; Mismatches 18; Indels 22; Gaps 2;
QY 488 LTEQESSPSHRSRTVSASSTGDLPAKAKTRAADLLVNPDPNADKIRVKIADLGNACW 547
Db 7 IPSQSQSSQNTYTIQS-----LIDN-----SNVRVKIADLGNACY 44
QY 548 VHKHFTEDIQTRQYSIEVLIGAGYSTPADINSTACMAFELATGDLPEPHSGEDYSRDE 607
Db 45 DVHHTFEDIQTRQYSIEVLIGAGYSTPADINSTACMAFELATGDLPEPHSGEDYSRDE 104
QY 608 DHIAHIE 615

Db 105 DHLAHIVD 112
RESULT 13
US-09-457-040B-13
; Sequence 13, Application US/09457040B
; Patent No. 6387641
; GENERAL INFORMATION:
; APPLICANT: Vertex Pharmaceuticals Incorporated
; APPLICANT: Bellon, Steve
; TITLE OF INVENTION: Crystallized P38 Complexes
; FILE REFERENCE: VPI/98-14
; CURRENT APPLICATION NUMBER: US/09/457,040B
; CURRENT FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Human
US-09-457-040B-13
Query Match 9.1%; Score 340.5; DB 3; Length 499;
Best Local Similarity 18.6%; Pred. No. 1e-15;
Matches 121; Conservative 66; Mismatches 127; Indels 335; Gaps 13;
QY 69 EDPADYCKGGYHPVKIGDLFNGRYHVRIRKLGWGHFSTVWLCD-MQGRFVAMKVKSQAQ 127
Db 144 EDDAE---GHLIYHVGDWLQERYEIVSTLGBGTGFRVVQCVDRRGGARVALKIKNVE 199
QY 128 HYETALDEIKLLKCVRESDDPNKMDVQLIDDFKISGMGIHVCMVFEVLGHLKWK 187
Db 200 KYKEAARLEINVLKINEKDPD--NKNLCVQMFDFYHG-----HMCISFELLGLSTPDF 253
QY 188 IIKSNVQGLPVRCKVSIIRQVLQGDYDLSKCKIHTDIKPNILMCDVDAVVRMAEA 247
Db 254 LKNNYLPYPHQVRHMAFQLCQAVKFLHDN-KLTHTDLKPNILFV-----299
QY 248 TEMQKAGAPPPSGSAVSTAPOQKPIGKISKNNKKLKKQKQKQKQKQKQKQKQKQKQKQKQ 307
Db 300 -----299
QY 308 AERKIIENITSAAPSNODGGEYCEVVKLTGTGLEAAEAETAKONGEAEDQEKEDAEK 367
Db 300 -----299
QY 368 ENIEKDEDDVDOELANIDPTWIESPKTNHENGPFSLQQLDDEDDDEDCPNPEYNL 427
Db 300 -----NSDYELT-----YNL 309
QY 428 DEPNAESDYTYSSSYEQFNGELPNGRHKIPESQPFESTLSFGSLSPVACGSLSEGSP 487
Db 310 EKKR-----313
QY 488 LTEQESSPSHRSRTVSASSTGDLPAKAKTRAADLLVNPDPNADKIRVKIADLGNACW 547
Db 314 -----DESVKSTAVRVVDFGSATF 333
QY 548 VHKHFTEDIQTRQYSIEVLIGAGYSTPADINSTACMAFELATGDLPEPHSGEDYSRDE 607
Db 334 DREHSTTVSTNHYRAPEVILELGWSQCDVWSIGCIIFEYVYVFTLFTQHD-----NR 387
QY 608 DHIAHIE 615
Db 388 EHLANMERILGPIPSMRIRKTKQKYFYRGLDWDENTSAGRYVRE--NCKPLRLYLTLS- 444
QY 648 KPSULFDVLVEKYGPHEDAAQFTFLIPMLEWPEKRSASAGECLRHFWL 696
Db 445 -----EABEHQFLDIESMLEYEPKRLITLGEALQHPF 478
RESULT 14

Search completed: January 19, 2005, 15:42:20
Job time : 44 secs

11110 rage Blank (uspio)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 19, 2005, 15:22:50 : Search time 160 Seconds
(without alignments)
1567.199 Million cell updates/sec

Title: US-10-799-676-2
Perfect score: 3742
Sequence: 1 MSSRKVLAIQARKRPKREK.....MVPEKASAGECLRHPLNS 699

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Genesep23Sep04:*

- 1: Genesep1980s:*
- 2: Genesep1990s:*
- 3: Genesep2000s:*
- 4: Genesep2001s:*
- 5: Genesep2002s:*
- 6: Genesep2003as:*
- 7: Genesep2003bs:*
- 8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3742	100.0	699	5	ABG32447 Human SR
2	3742	100.0	699	7	ADJ37689 Human kin
3	3626	96.9	688	6	Aao26722 SR protei
4	3626	96.9	688	8	ADJ96645 Human SRP
5	3622	96.8	675	6	Aao26721 SR protei
6	3620	96.7	688	2	AAY27053 Human pro
7	3586	95.8	686	5	Aau80373 Human cel
8	3586	95.8	686	6	Aae34823 Protein #
9	3586	95.8	686	8	ADOL19347
10	3395.5	90.7	681	7	ADE59481 Rat Prote
11	3117	83.3	1070	4	ABG02155
12	2070.5	55.3	655	2	Aaw06556 Serine ki
13	2050	54.8	654	6	Aao26720 SR protei
14	1890	50.5	567	8	ADe28302 Human KRP
15	1882	50.3	533	6	Aao26723 SR protei
16	1882	50.3	533	6	Aao26724 SR protei
17	1882	50.3	533	7	ADe31691 Human 142
18	1882	50.3	533	8	ADI29289 Human MAR
19	1882	50.3	533	8	ADQ18730 Human sof
20	1865.5	49.9	532	4	AAe5681 Novel pro
21	1338	35.8	338	6	AAO26725 SR protei
22	1337	35.7	334	8	ADN99237 Novel hum
23	1298.5	34.7	880	4	ABB71719 Drosophil
24	1294.5	34.6	748	4	ABe2581 Drosophil
25	1075	28.7	538	3	AAG12830 Arabidops

26	1075	28.7	578	3	AAG12829	Aag12829 Arabidops
27	1068	28.5	538	3	AAG45141	Aag45141 Arabidops
28	1068	28.5	577	3	AAG45140	Aag45140 Arabidops
29	943	25.2	790	4	ABB63932	Abb63932 Drosophil
30	852	22.8	4134	2	AAY31946	Aay31946 Plasmodiu
31	841	22.5	452	3	AAG12831	Aag12831 Arabidops
32	835	22.3	297	3	AAY76748	Aay76748 Human pro
33	835	22.3	297	4	AAE06206	Aae06206 Human pro
34	835	22.3	297	5	ABB84433	Abb84433 Human pro
35	834	22.3	452	3	AAG45142	Aag45142 Arabidops
36	817	21.8	154	4	ABB38855	Abb38855 Peptide #
37	817	21.8	154	4	AAM32330	Aam32330 Peptide #
38	817	21.8	154	4	ABB23863	Abb23863 Protein #
39	817	21.8	154	4	AAM72065	Aam72065 Human bon
40	817	21.8	154	4	AAM59499	Aam59499 Human bra
41	817	21.8	154	4	ABG53749	Abg53749 Human liv
42	817	21.8	154	5	ABG41880	Abg41880 Human pep
43	720	19.2	187	4	AAE63273	Aae63273 Human bre
44	720	19.2	187	4	AAE63384	Aae63384 Human bre
45	666	17.8	386	3	AAG18143	Aag18143 Arabidops

ALIGNMENTS

RESULT 1
ABG32447
ID ABG32447 standard; protein; 699 AA.
XX AC ABG32447;
XX DT 20-NOV-2002 (first entry)
XX DE Human SR protein-specific kinase 2, SRPK2.
XX KW Human; kinase; SRPK2; SR protein-specific kinase 2; enzyme.
XX OS Homo sapiens.
XX PN US2002094560-A1.
XX PD 18-JUL-2002.
XX PF 16-JAN-2001; 2001US-00759359.
XX PR 16-JAN-2001; 2001US-00759359.
XX PA (ABUT/) ABU-THREIDEH J.
XX PA (GONG/) GONG F.
XX PA (KERC/) KETCHUM K A.
XX PA (DFRA/) DI FRANCESCO V.
XX PA (BEAS/) BEASLEY E M.
XX PI Abu-Threideh J, Gong F, Ketchum KA, Di Francesco V, Beasley EM;
XX DR WPI; 2002-681805/73.
XX DR N-PSDB; ABS52846.
XX PT New SR protein-specific kinase 2 peptides and nucleic acid sequences,
XX PT useful as models for developing human therapeutic targets, in identifying
XX PT therapeutic proteins, and in identifying agents that modulate kinase
XX PT activity.
XX PT Claim 1; Fig 2; 56pp; English.
XX CC The invention relates to an isolated human SR protein-specific kinase 2
XX CC (SRPK2) peptide. The SR protein-specific kinase 2 peptide and nucleic
XX CC acid sequences can be used as models for the development of human
XX CC therapeutic targets, aid in the identification of therapeutic proteins,
XX CC and as targets for the development of human therapeutic agents that
XX CC modulate kinase activity in cells and tissues that express the kinase.
XX CC These may further be used as query sequences to perform a search against
XX CC sequence databases to identify other family members or related sequences.

CC The peptides can also be used to raise antibodies or to elicit another
CC immune response, as markers for tissues in which the corresponding
CC protein is preferentially expressed, to identify the binding
CC partner/ligand to develop a system to identify inhibitors of the binding
CC interaction, and in pharmacogenomic analysis. The nucleic acids are
CC useful as probes or primers, for expressing antigenic portions of the
CC proteins, for constructing vectors, host cells or transgenic animals
CC expressing the nucleic acids and peptide, for monitoring the
CC effectiveness of modulating compounds on the expression or activity of
CC the kinase gene in clinical trials or in treatment regimen, and as
CC antisense constructs to control kinase gene expression. The present
CC sequence represents the amino acid sequence of human SRPK2
XX
XX
SQ Sequence 699 AA;

Query Match 100.0%; Score 3742; DB 5; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.1e-268;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSRKVLAIQARKRPKREKPKPEQOKAPLVPPPPPPPPPPPPPPPPPPPPPEEEI 60
Db 1 MSSRKVLAIQARKRPKREKPKPEQOKAPLVPPPPPPPPPPPPPPPPPPPPPEEEI 60

QY 61 LGSDDDEEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCWDMQGRFVAM 120
Db 61 LGSDDDEEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCWDMQGRFVAM 120

QY 121 KVVKSQAQHYTETALDEIKLLKCVRESDDPNKMWVOLIDDYKISGMNGHVCWVFEVL 180
Db 121 KVVKSQAQHYTETALDEIKLLKCVRESDDPNKMWVOLIDDYKISGMNGHVCWVFEVL 180

QY 181 GHLLKWIILKSNYQGLPVRCKSIIRQVLQGLDYLHSCKIIHTDIKPENILCMVDDAYV 240
Db 181 GHLLKWIILKSNYQGLPVRCKSIIRQVLQGLDYLHSCKIIHTDIKPENILCMVDDAYV 240

QY 241 RMAAEATWQKAGAPPPSGSASTAPQOKPIGKISKNKKLKKQKQAELEKRLQE 300
Db 241 RMAAEATWQKAGAPPPSGSASTAPQOKPIGKISKNKKLKKQKQAELEKRLQE 300

QY 301 IELEAREARKIIEENITSAAPSDODGYCEPVKLTGLEAAEAETAKONGEAEDQ 360
Db 301 IELEAREARKIIEENITSAAPSDODGYCEPVKLTGLEAAEAETAKONGEAEDQ 360

QY 361 EKEDAENIEKDDDDVQELANIDPTWIESPKTNGHIENGPFSLQQLDDEDDDEDCP 420
Db 361 EKEDAENIEKDDDDVQELANIDPTWIESPKTNGHIENGPFSLQQLDDEDDDEDCP 420

QY 421 NPEEYNLDENPNAESDYTSYSSYEQFNGELPNGRHKIPESQPFESTSLFSGSLPVACGS 480
Db 421 NPEEYNLDENPNAESDYTSYSSYEQFNGELPNGRHKIPESQPFESTSLFSGSLPVACGS 480

QY 481 VLSEGSPLTEQESSPSHDSRTVSASTGDLPAKTRAADLIVNPLDPNADKIRVKIA 540
Db 481 VLSEGSPLTEQESSPSHDSRTVSASTGDLPAKTRAADLIVNPLDPNADKIRVKIA 540

QY 541 DLGNACWVKHFTEDIQYRSIEVLIGAGYSTPADIWSTACMAFELATGDIYLFPHSG 600
Db 541 DLGNACWVKHFTEDIQYRSIEVLIGAGYSTPADIWSTACMAFELATGDIYLFPHSG 600

QY 601 EDYSRDEDHIAHIELLGSIPRFALSGKYSREFFNRRGELRHITKLPWSLFDVLVEKY 660
Db 601 EDYSRDEDHIAHIELLGSIPRFALSGKYSREFFNRRGELRHITKLPWSLFDVLVEKY 660

QY 661 GWPHEAQAQTFDILPMLNVEPKRASAGECLRHPLWNS 699
Db 661 GWPHEAQAQTFDILPMLNVEPKRASAGECLRHPLWNS 699

RESULT 2
ADJ37689
ID ADJ37689 standard; protein; 699 AA.
XX
AC ADJ37689;

XX 06-MAY-2004 (first entry)
DT Human kinase protein.
DE
DE Kinase protein; drug screening assay; gene therapy;
KW pharmacogenomic analysis; testis; nervous tissue; fetal; lung;
KW brain anaplastic oligodendroglioma; lung carcinoma tissue;
KW soft tissue leiomyosarcoma; ovary tumour tissue; germ cell tumour tissue;
KW transgenic animal; human; enzyme.
XX
OS Homo sapiens.
XX
XX US2003175927-A1.
FN
PD 18-SEP-2003.
XX
XX 31-JUL-2002; 2002US-00207973.
PF
XX 16-JAN-2001; 2001US-00759359.
PR
XX (APPL-) APPLERA CORP.
PA
XX Abu-Threideh J, Gong F, Ketchum KA, Di Francesco V, Beasley EM;
PI WPI; 2003-898544/82.
XX N-PSDB; ADJ37688.
DR
XX New peptides related to kinase protein subfamily useful for treating
XX disorders associated with abnormal expression of kinase protein in
XX testis, nervous tissue, fetal, lung, ovary tumor tissue.
XX
XX Claim 1; SEQ ID NO 2; 102pp; English.
PS
CC The present invention relates to kinase protein and nucleotides encoding
CC them. The invention is useful in drug screening assays, tissue typing,
CC gene therapy and pharmacogenomic analysis. They are also useful in
CC treating disorders associated with the absence of, inappropriate, or
CC unwanted expression of kinase protein in testis, nervous tissue, fetal,
CC lung, brain anaplastic oligodendroglioma, lung carcinoma tissue, soft
CC tissue leiomyosarcoma, ovary tumour tissue, or germ cell tumour tissue.
CC The invention are useful as models for the development of human
CC therapeutic targets, aid in the identification of therapeutic proteins
CC and serve as targets for the development of human therapeutic agents that
CC modulate protease activity in cells and tissues that express the kinase
CC peptide. The invention is also useful in producing a kinase protein or
CC peptide, and non-human transgenic animals. The present sequence is human
CC kinase protein.
XX
SQ Sequence 699 AA;

Query Match 100.0%; Score 3742; DB 7; Length 699;
Best Local Similarity 100.0%; Pred. No. 1.1e-268;
Matches 699; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSRKVLAIQARKRPKREKPKPEQOKAPLVPPPPPPPPPPPPPPPPPPPPPEEEI 60
Db 1 MSSRKVLAIQARKRPKREKPKPEQOKAPLVPPPPPPPPPPPPPPPPPPPPPEEEI 60

QY 61 LGSDDDEEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCWDMQGRFVAM 120
Db 61 LGSDDDEEQEDPADYCKGGYHPVKIGDLFNGRYHVIRKLGWGHFSTVWLCWDMQGRFVAM 120

QY 121 KVVKSQAQHYTETALDEIKLLKCVRESDDPNKMWVOLIDDYKISGMNGHVCWVFEVL 180
Db 121 KVVKSQAQHYTETALDEIKLLKCVRESDDPNKMWVOLIDDYKISGMNGHVCWVFEVL 180

QY 181 GHLLKWIILKSNYQGLPVRCKSIIRQVLQGLDYLHSCKIIHTDIKPENILCMVDDAYV 240
Db 181 GHLLKWIILKSNYQGLPVRCKSIIRQVLQGLDYLHSCKIIHTDIKPENILCMVDDAYV 240

QY 241 RMAAEATWQKAGAPPPSGSASTAPQOKPIGKISKNKKLKKQKQAELEKRLQE 300
Db 241 RMAAEATWQKAGAPPPSGSASTAPQOKPIGKISKNKKLKKQKQAELEKRLQE 300

[illegible]

XX Chien D, Jin P, Hawkins PR, Baughn MR, Becha SD, Chang H;
PI Ding L, Elliott VS, Emerling BM, Gandhi AR, Gietzen KJ, Griffin JA;
PI Gururajan R, Hafalia AJA, Ison CH, Kable AE, Khare R, Lee SY;
PI Lee EA, Lu Y, Marquis JP, Lehr-Mason PM, Ramkumar J, Richardson TW;
PI Swarnakar A, Tran UK, Chawla NK, Yao MG, Yue H, Bhatia U;
PI Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;
XX WPI: 2004-011523/01.
DR N-PSDB; ADE28354.
XX
XX New human kinases and phosphatases, and polynucleotides encoding them,
PT useful for treating, preventing or diagnosing e.g. cell proliferative
PT disorders, inflammatory, autoimmune, viral, bacterial, parasitic or
PT fungal diseases.
XX
PS Claim 1; SEQ ID NO 13; 340pp; English.
XX
XX The invention relates to a novel isolated kinase and phosphatase (KPP)
CC polypeptide. The polypeptide of the invention demonstrates hepatotropic,
CC antiarteriosclerotic, antiporiatic, cytostatic, haemostatic, muscular,
CC cerebroprotective, nootropic, ophthalmological, anticonvulsant,
CC vasotropic, neuroprotective, antiparkinsonian, antiasthmatic,
CC antianemic, antiasthmatic, antidiabetic, antiinflammatory, osteopathic,
CC antiarthritic, antirheumatic, dermatological, virucide, antibacterial,
CC fungicide, antiparasitic, protozoicidal, antihelminthic, antigout,
CC cardiovascular, antiarteriosclerotic and immunosuppressive activities.
CC The KPP polypeptides may be useful for diagnosing, treating or preventing
CC cell proliferative disorders including cirrhosis, hepatitis,
CC arteriosclerosis, psoriasis, primary thrombocytopenia and cancer,
CC developmental disorders such as renal tubular acidosis, Becker's muscular
CC dystrophy, gonadal dysgenesis, hypothyroidism or seizures, neurological
CC disorders e.g. Pick's disease, cataract, epilepsy, ischaemic
CC cerebrovascular disease, stroke, Alzheimer's disease, Parkinson's disease
CC or dementia, autoimmune or inflammatory disorders including AIDS,
CC allergies, anaemia, asthma, diabetes mellitus, bronchitis, osteoporosis,
CC osteoarthritis, rheumatoid arthritis, contact dermatitis or gout and
CC lipid disorders such as cholestasis, Gaucher's disease, diabetes,
CC atherosclerosis or liver disease, as well as viral, bacterial, fungal,
CC parasitic, protozoan or helminthic infections and trauma. Furthermore,
CC the polypeptide may be utilised during gene therapy procedures. The
CC current sequence is that of the human KPP protein of the invention.
XX
SQ Sequence 567 AA;
Query Match 50.5%; Score 1890; DB 8; Length 567;
Best Local Similarity 58.1%; Pred. No. 2.2e-131;
Matches 378; Conservative 57; Mismatches 90; Indels 126; Gaps 12;
QY 52 TP-PEPEEILGSDDEQEDPADYCKGGYHPVKIGDLNFRVYHVRKLGWGHFSTWLCW 110
DB 38 TPVPQMLQGLGSDDEQEDPDYCKGGYHPVKIGDLNFRVYHVRKLGWGHFSTWLCW 97
QY 111 DMOGRFVAMKVKAQHVYETALDEIKLKCVRSDPSDPKMDVMVVLIDDFKISGNG 170
DB 98 DIQRKRFVAMKVKAQHVYETALDEIKLKCVRSDPSDPKRETIIVQIDDFRISGNG 157
QY 171 IHVCMVFVGLHLLKWIKSNYQGLPVRCVKSIIRQVLQGLDYHLSKCKIHTDKPEN 230
DB 158 VHVCVMVLEVLGHLKWIKSNYQGLPVRCVKSIIRQVLHGLDYHLSKCKIHTDKPEN 217
QY 231 ILMCVDDAYVRMAEATEWQAGAPPSPGSAVSTAPQO-KPIGKISNKKKLLKKOKR 289
DB 218 ILLCVGDYIRLAAEATEWQAGAPPSPGSRVSTAPQVLTQGLSKNKKRKKMRKQ 277
QY 290 QAELEKRLQETEEELEREAERKIIENITSAPSNDQGEYCEPVKLTGTGLEEAET 349
DB 278 QKRLLEERLDIQR-----EAEARAT 299
QY 350 AKDNGEAEQEEKEDAEKENIEKEDDQDLANIDPTWIESPKTNGHIENGPFSLQQL 409
DB 300 -----QAEGLSLDGGSGSTSSGGCHP-----GGARAGP----- 329

QY 410 DDEDDDEDCNPEYNLDPENAESDYTYSSSYEQFNGELPNGRHKIPESQFPERSTSLF 469
DB 330 -----SPASSSPAP-----GGRSLSAGSQTSFGSGSLF 358
QY 470 SGLSEPVACGVLSESGSLTEQEESSPSHRSRTVSASSTGDL--PKAKTRAADLLVNPL 527
DB 359 S-----PASC-SILSGSS--NORE-----TGGLSPSTPFGASNLVNPL 395
QY 528 DPRADKIRVKIADLGNACWVHKHFTEDIOTROYRSIEVLIGAGYSTPADINSTACMAFE 587
DB 396 EPQADNKKIKIADLGNACWVHKHFTEDIOTROYRAVEVLIGAGYGGPPADIWSTACMAFE 455
QY 588 LATGDLPEPHSGEDYSRDEDHIAHIELGSIIPRHFALSGKYSREFFNRRGELRHITKL 647
DB 456 LATGDLPEPHSGEDYSRDEDHIAHIELGDIPPAPALSGKYSREFFNRRGELRHITKL 515
QY 648 KPWSLFDVLVEKYGWPHEDAQAQTFDLIPMLEMVPKESASAGECLRHHPWLN 698
DB 516 KHWGLYEVLMKYEWPLEQATQPSAFLPMPMEYIPEKASAAADCLQHPWLN 566
RESULT 15
ID AAO26723
XX AAO26723 standard; protein; 533 AA.
XX AAO26723;
XX
DT 27-MAR-2003 (first entry)
XX SR protein-specific kinase-1 protein, SEQ ID No 16.
XX Cytostatic; p53 pathway-modulating agent; SR protein; cancer; apoptosis;
KW lung cancer; breast cancer; serine/arginine protein-specific kinase;
KW colon cancer; ovarian cancer; SRPK; cell proliferation; human.
OS Homo sapiens.
PN WO200299427-A1.
XX 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017525.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 15-FEB-2002; 2002US-0357253P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
XX WPI: 2003-156865/15.
XX
PT Identifying candidate p53 pathway-modulating agents useful as therapeutic
PT targets for disorders related with defective p53 function, by screening
PT for agents modulating serine/arginine protein-specific kinase activity.
XX
PS Claim 13; Page 130-132; 137pp; English.
XX
XX The invention relates to a novel method for identifying candidate p53
CC pathway-modulating agents. The novel method comprises screening for
CC agents that modulate the activity of a serine/arginine protein-specific
CC kinase. The invention provides methods for utilising p53 modifier genes
CC and polypeptides to identify candidate therapeutic agents that can be
CC used in the treatment of disorders associated with defective p53
CC function. The methods are also useful for modulating a p53 pathway in a
CC mammalian cell, or for diagnosing or treating a disease associated with
CC defective p53 function, e.g. cancers such as breast cancer, colon cancer,
CC lung cancer or ovarian cancer. The serine/arginine protein-specific
CC kinase (SRPK) polypeptides and nucleic acids are useful for identifying
CC and testing agents that modulate SRPK function. The animal models are
CC useful for in vivo assays to test the activity of a candidate p53-
CC modulating agent, or to assess the role of SRPK in a p53 pathway process


```
QY 877 TTATTGGAGAGCGCTCGCAGGATAGAAAGATTGGAGCGAGAGCTGAAAGGAAATA 936
Db 61 TTATTGGAGAGCGCTCGCAGGATAGAAAGATTGGAGCGAGAGCTGAAAGGAAATA 120
QY 937 ATAGAAGAAAACATCACCTCAGCTGCACCTTCCAAATGACAGGATGGCGAATCTGCCCA 996
Db 121 ATAGAAGAAAACATCACCTCAGCTGCACCTTCCAAATGACAGGATGGCGAATCTGCCCA 180
QY 997 GAGGTGAACCTAATAACCAACAGGATTAGAGAGCGGCTGAGGCGAGACACTGCAAGGAC 1056
Db 181 GAGGTGAACCTAATAACCAACAGGATTAGAGAGCGGCTGAGGCGAGACACTGCAAGGAC 240
QY 1057 ATGCTGAGCTGAGGACGAGGAGAGAAAGAGATGCTGAGAAAGAAAACATTGAAAAA 1116
Db 241 AATGCTGAGCTGAGGACGAGGAGAGAAAGAGATGCTGAGAAAGAAAACATTGAAAAA 300
QY 1117 GATGAAGATGATTAGATCAGAACTTGCAGACATAGACCCCTACCTGATAGAAATCACCT 1176
Db 301 GATGAAGATGATTAGATCAGAACTTGCAGACATAGACCCCTACCTGATAGAAATCACCT 360
QY 1177 AAAACCAATGGCCATATTGAGAAATGGCCCATCTCACTGGAGCAGCAACTGGACGATGAA 1236
Db 361 AAAACCAATGGCCATATTGAGAAATGGCCCATCTCACTGGAGCAGCAACTGGACGATGAA 420
QY 1237 GATGATGATGAAGAGACTGCCAAATCTGAGGAATATAATCTTGTATGAGCCAAATGCA 1296
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QY 1297 GAAAGTGATTACACATATAGCAGCTCTATGAACAATCAATGGTGAATTCGCAATGGA 1356
Db 481 GAAAGTGATTACACATATAGCAGCTCTATGAACAATCAATGGTGAATTCGCAATGGA 540
QY 1357 CGACATAAAATTCGAGTACAGTTCCAGAGTTTCCACCTCGTTCTCTCGATCC 1416
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QY 1417 TTGAACCTGTGCGCTCGCGCTCTGTGCTTCTGAGGATCACCACTTACTGAGCAAGAG 1476
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Db 1021 ATCATAGAGTGTAGGAGTATTTCCAGGCACTTTGCTCTATCTGGAATAATTTCTCG 1080
QY 1897 GAATTTCTTCAATCGCAGAGGAGAACTGCGACACATACCAAGCTGAAGCCCTCGAGCCTC 1956
Db 1081 GAATTTCTTCAATCGCAGAGGAGAACTGCGACACATACCAAGCTGAAGCCCTCGAGCCTC 1140
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QY 1957 TTTGATGTACTTGTGAAAAAGTATGCTGGCCCCCATGAAGATCTGCACAGTTTACAGAT 2016
Db 1141 TTTGATGTACTTGTGAAAAAGTATGCTGGCCCCCATGAAGATCTGCACAGTTTACAGAT 1200
QY 2017 TTCTGTATCCCGATGTAGAAATGGTTCCAGAAAAACGAGCCTCAGCTGGCGAATGCCTT 2076
Db 1201 TTCTGTATCCCGATGTAGAAATGGTTCCAGAAAAACGAGCCTCAGCTGGCGAATGCCTT 1260
QY 2077 CGGCATCCTTGGTTGAATCTCT 2097
Db 1261 CGGCATCCTTGGTTGAATCTCT 1281

RESULT 2
BX463511 995 bp mRNA linear EST 05-MAY-2004
LOCUS BX463511 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CS0DN003YA14 5-PRIME, mRNA sequence.
ACCESSION BX463511
VERSION BX463511.2 GI:47056867
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1. (bases 1 to 995)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 22, 2003 this sequence version replaced gi:31027556.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to this cluster, see
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DN003BA07QP1&c=4027.r.

FEATURES
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/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
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Best Local Similarity 99.4%; Pred. No. 7.6e-236;
Matches 986; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 820 AAAATATCTTAAACACAAAGAAAACCTGAAAAGAAAACAGAGAGCGGCTGAGTTA 879
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QY 880 TTGGAGAGCGCTCGCAGGATAGAGAAATTTGGAGCGAGAGCTGAAAGGAAAATAATA 939
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QY 940 GAAGAAAACATCACCTCAGCTGCACCTTCCATATGACAGGATGGCGAATCTGCCAGAG 999
Db 125 GAAGAAAACATCACCTCAGCTGCACCTTCCATATGACAGGATGGCGAATCTGCCAGAG 184
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Qy	1183	AATGGCCATATTGAGAAATGGCCCAATTTCTCACTGGAGCAGCAACTTGGACGATGAAGATGAT	1242
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Qy	1243	GATGAAGAAGACTGCCCAATTCCTGAGGAATATAATCTTGATGAGGCCAAATTCGAGAAAGT	1302
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Qy	1303	GATTACACATATAGCAGCTCCTATGAAACAATCAATGGTGAATTCGCAATTGGACGACAT	1362
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Qy	1423	CCTGTGGCCTCGGGCTCTGTCTTTCTGTGAGGGATCACCATTTACTGAGCAAGAGGAGGC	1482
Db	901	CCTGTGGCCTCGGG-TCTGTGCTTTCTGTGAGGGAT-MCCMCTTACTGTGRC-AGRGAGAGC	957
Qy	1483	AGTCATATCCCATGACAGAAGCA	1504
Db	958	AGTCATATCCCGACAGAAAMRCA	979

RESULT	4
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LOCUS	BM464185 1108 bp linear EST 05-FEB-2002
DEFINITION	AGENCOURT_6438899 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5535256 5' , mRNA sequence.

BM464185
 BM464185.1 GI:18513227
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1108)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 plate: LLAM13223 row: a column: 17
 high quality sequence stop: 787.

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FEATURES
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/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."
ORIGIN
Query Match 38.9%; Score 816.2; DB 4; Length 1108;
Best Local Similarity 99.6%; Pred. No. 2e-195;
Matches org. Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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[illegible]

RESULT 5	REFERENCE
BU166874	AUTHOR
LOCUS	TITLE
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANIZATION	

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Db <td>661</td> <td>TTGTTTGAACCCACATTTCTGGGGAAGACTATTTCAGAGACGAAGACACATAGCCCAATC</td> <td>720</td>	661	TTGTTTGAACCCACATTTCTGGGGAAGACTATTTCAGAGACGAAGACACATAGCCCAATC	720
Qy <td>1840</td> <td>ATGAGAGCTGCTAGGCAAGTATTTCCAAAGCACTTTGGCTCTATCTCGAAATAATTTCTCGGAA</td> <td>1899</td>	1840	ATGAGAGCTGCTAGGCAAGTATTTCCAAAGCACTTTGGCTCTATCTCGAAATAATTTCTCGGAA	1899
Db <td>721</td> <td>ATAAAGCTGCTAGGCAAGTATTTCCAAAGCACTTTGGCTCTATCTCGAAATAATTTCTCGGGA</td> <td>780</td>	721	ATAAAGCTGCTAGGCAAGTATTTCCAAAGCACTTTGGCTCTATCTCGAAATAATTTCTCGGGA	780
Qy <td>1900</td> <td>TTCTTCAATCGCAGA--GGAGAACTGCGACATCAACCA--CCTGAAGCCCTGGAGCCT</td> <td>1955</td>	1900	TTCTTCAATCGCAGA--GGAGAACTGCGACATCAACCA--CCTGAAGCCCTGGAGCCT	1955
Db <td>781</td> <td>TTCTCTCATCCCAAGAGGAAATATGCGACCATCACCCAAAGCTGGAAGCCCCCGAACC</td> <td>840</td>	781	TTCTCTCATCCCAAGAGGAAATATGCGACCATCACCCAAAGCTGGAAGCCCCCGAACC	840
Qy <td>1956</td> <td>CTTTGATGTACTTTGTGGAATA 1976</td> <td></td>	1956	CTTTGATGTACTTTGTGGAATA 1976	
Db <td>841</td> <td>CTTTGATGGACTTTGGGGAAA 861</td> <td></td>	841	CTTTGATGGACTTTGGGGAAA 861	
RESULT 6			
AUI24932			
LOCUS	AUI24932 NT2RM4	Homo sapiens cDNA clone NT2RM4000760 5', mRNA	
DEFINITION	AUI24932	828 bp mRNA linear EST 01-AUG-2002	
ACCESSION	AUI24932	sequence.	
VERSION	AUI24932.1	GI:10949648	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S., Isogai, T., Isogai, T.		
TITLE	HRI human cDNA project (Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S., Isogai, T.)		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3975 Fax: 81-438-52-3986 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.		
FEATURES			
source	1. .828	Location/Qualifiers	
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/clone="NT2RM4000760"		
	/cell_type="teratocarcinoma"		
	/cell_line="NT2"		
	/clone_lib="NT2RM4"		
	/notes="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal precursor cells"		
ORIGIN			
Query Match	36.2%	Score 759.2; DB 1; Length 828;	
Best Local Similarity	98.8%	Pred. No. 5.2e-181;	
Matches 795; Conservative	0; Mismatches 16;	Indels 4; Gaps 3;	
Qy	1247	AAGAAGACTGCCAAATCTTGAGCAATATAATCTTGATGAGCCAAATGCAGAAAGTGATT	1306
Db	14	AAGAAGACTGCCAAATCTTGAGCAATATAATCTTGATGAGCCAAATGCAGAAAGTGATT	73
Qy	1307	ACACATATAGCAGCTCCTATGAACAAATTCATCGGTGAATTCGCAATGGACGACATAAAA	1366

QY 1414 TCCTTAGAACCTGTGGCTCGGCTCTGTGCTTTCTGAGGGATCACCACCTTACTGAGCAA 1473
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 Db 661 TCCTTAGAACCTGTGGCTCGGCTCTGTGCTTTCTGAGGGATCACCACCTTACTGAGCAA 720
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 QY 1474 GA-GGAGACAGTCCATCCCATGACAGAAGCAGAAC-GGTTTTCAGCTCCAG--TACTGG 1529
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 Db 721 GAGGAGAGACAGTCCATCCCTGACAGAAGCCGAGCGGTTTTCAGCTCCAGGACTGGG 780
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 QY 1530 GGATTTGCCAAA--GCAAAAACCGGCGAGCTGACTTGT--GGTGAATCCCTGGATC 1585
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 Db 781 GGATTTGCCAAAAGCAAAAACCCCGGCGAGCTGACCGGTTTGGTGAATCCCTGGATC 840
 |||||
 QY 1586 CGC-GGAATGCAGATAAAA--TTAGAGTAAAAATTG-CTGACCTGGGAAA--TGCTTGT 1639
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 Db 841 CCGGAGAGCGAGATAAAATTAGAGTAAAAATTGCTGACCTGAGAAAATGCTTGGTG 900
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 QY 1640 GGGTGCATAAACACTTTCACGGAA 1662
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 Db 901 GGGGCGATAAACCTTTCGGAA 923
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RESULT 8
 BX423898
 LOCUS
 DEFINITION BX423898 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
 CS0DN003YA14 5-PRIME, mRNA sequence.
 ACCESSION BX423898
 VERSION BX423898.2 GI:46927093
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 900)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 13, 2003 this sequence version replaced gi:30643492.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 This sequence belongs to sequence cluster 4027.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?S=CSIAN001ZE08QPl&c=4027.r.

http://www.genoscope.cns.fr/cdna?S=CSIAN001ZE08QPl&c=4027.r.

FEATURES
 source
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DN003YA14"
 /tissue_type="ADULT BRAIN"
 /dev_stage="adult"
 /clone_lib="Homo sapiens ADULT BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN
 Query Match 35.4%; Score 741.8; DB 5; Length 900;
 Best Local Similarity 97.0%; Pred. No. 1.4e-176;
 Matches 808; Conservative 2; Mismatches 14; Indels 9; Gaps 5;
 QY 820 AAAATATCTAAAAACAAAAGAAAAAAGTGAAGAAAAAGAAAGAGGCGGCTGAGTTA 879
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 Db 5 AAATATCTAAAAACAAAAGAAAAAAGTGAAGAAAAAGAAAGAGGCGGCTGAGTTA 64
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QY 880 TTGGAGAGC--GCCTGAGGAGATAGAGAAATTTGGAGCGAGAGCTGAAAGAAATAA 937
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 Db 65 TTGGAGAGC--GCCTGAGGAGATAGAGAAATTTGGAGCGAGAGCTGAAAGAAATAA 124
 |||||
 QY 938 TAGAAGAAAAACATCACTCAGCTGCACTTCCAATGACAGGATGGCGAATCTGCCCGAG 997
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 Db 125 TAGAAGAAAAACATCACTCAGCTGCACTTCCAATGACAGGATGGCGAATCTGCCCGAG 184
 |||||
 QY 998 AGGTGAAACTAAAAACAAACAGAGTTAGAGAGCGGCTGAGCGAGAGATGCAAAAGACA 1057
 |||||
 Db 185 AGGTGAAACTAAAAACAAACAGAGTTAGAGAGCGGCTGAGCGAGAGATGCAAAAGACA 244
 |||||
 QY 1058 ATGGTGAAGCTGAGACACGAGGAGAGAGATGCTTGAGAAAGAAACATTTGAAAAG 1117
 |||||
 Db 245 ATGGTGAAGCTGAGACACGAGGAGAGAGATGCTTGAGAAAGAAACATGAAAAG 304
 |||||
 QY 1118 ATGAAGATGATGTAGATCAGGAATTTGCGAAACATAGACCTACCTGCGATAGAAATCACCTA 1177
 |||||
 Db 305 ATGAAGATGATGTAGATCAGGAATTTGCGAAACATAGACCTACCTGCGATAGAAATCACCTA 364
 |||||
 QY 1178 AAACCAATGGCCATATTGAGAAATGCCCATTTCTACTGGAGCAGCAACTGGAGTGAAG 1237
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 Db 365 AAACCAATGGCCATATTGAGAAATGCCCATTTCTACTGGAGCAGCAACTGGAGTGAAG 424
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 QY 1238 ATGATGATGAAGAAGACTGCCCCAAATCCTGAGGAATATAATCTTGATGAGCCAAATGCGAG 1297
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 Db 425 ATGATGATGAAGAAGACTGCCCCAAATCCTGAGGAATATAATCTTGATGAGCCAAATGCGAG 484
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 Db 485 AAGTGATTTACACATATATAGCAGCTCCTATGAAACAATCAATGGTGAATTTGCCAAATGGA 544
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 QY 1357 CGACATAAAATTTCCCGAGTTCACAGTTTCCAGAGTTTCCACCTCGTGTGTTCTCTGGATCC 1416
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 Db 545 CGACATAAAATTTCCCGAGTTCACAGTTTCCAGAGTTTCCACCTCGTGTGTTCTCTGGATCC 604
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 QY 1417 TTAGAACCTGTGGCTCGGCTCTGTGCTTTCTGAGGATCACCCTTACTGAGCAGAG 1476
 |||||
 Db 605 TTAGAACCTGTGGCTCGGCTCTGTGCTTTCTGAGGATCACCCTTACTGAGCAGAG 664
 |||||
 QY 1477 GAGACAGTCCATCCATGACAGAGAGAGAGCGTTTTCAGCTCCAGTACTGGGATTTG 1536
 |||||
 Db 665 GAGACAGTCCATCCATGACAGAGAGAGAGCGTTTTCAGCTCCAGTACTGGGATTTG 724
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 QY 1537 CCAAAGCAAAACCCGGGCGAGCTGACTTTGTTGGTGAATCCCTCGATCCCGGGAATGCA 1596
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 Db 725 CCAAAGCAAAACCCGGGCGAGCTGACTTTGTTGGTGAAT-CCCTGGATCCGCGG-ATGCA 782
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 QY 1597 GATAAAATTAGAGTAAAAATTCCTGACCTGGGAAATGCTTGTGGTGCATTA 1649
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 Db 783 GATAAAATTAGAGTAAAAATTTG----ACTKGGGAATGCTTGTGGTGCATTA 831
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RESULT 9
 BX442846
 LOCUS
 DEFINITION BX442846 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 CS0DF038Y110 5-PRIME, mRNA sequence.
 ACCESSION BX442846
 VERSION BX442846.2 GI:47037734
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 960)
 Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On May 22, 2003 this sequence version replaced gi:31018541.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4027.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CS0DF038BE05QP1&c=4027.r.

FEATURES

Location/Qualifiers
1..960
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF038Y110"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Query Match 35.2%; Score 739; DB 5; Length 960;
Best Local Similarity 94.5%; Pred. No. 7.3e-176;
Matches 757; Conservative 25; Mismatches 16; Indels 3; Gaps 2;
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DB 154 TTCAGAAAGCCGGAGCCTCAACAGAAAGCTCTTTAGTTCCTCTCTCCACCCGCCACC 213
QY 123 ACCACACC-ACCGCCACTTTGCCAGACCCACACCCCGGAGCCAGAGGAGATC 180
DB 214 ACCACACCAGCGCCACCTTTGCCAGACCCACACCCCGGAGCCAGAGGAGATC 273
QY 181 CTGGGATCAGATGATGAGGAGCAAGAGACCTCTGGGACTACTGCAAAAGGTGGATATCAT 240
DB 274 CTGGGATCAGATGATGAGGAGCAAGAGACCTCTGGGACTACTGCAAAAGGTGGATATCAT 333
QY 241 CCAAGTAAATTTGGAGACCTTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGG 300
DB 334 CCAAGTAAATTTGGAGACCTTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGG 393
QY 301 GGGCACTTCTACTGCTGCTGGTGTCTGGGATATGCGGGGAAAGATTTGTCGAATG 360
DB 394 GGGCACTTCTACTGCTGCTGGTGTCTGGGATATGCGGGGAAAGATTTGTCGAATG 453
QY 361 AAAGTTGTAAGAGTCCCGACATTTATACGGAGACAGCCTTGGATGAAATAAAATTTGCTC 420
DB 454 AAAGTTGTAAGAGTCCCGACATTTATACGGAGACAGCCTTGGATGAAATAAAATTTGCTC 513
QY 421 AAATGTTTCGAGAAAGTATCCAGTATGCCAGATGCCAAACAAAGACATGGTGTCCAGTCAAT 480
DB 514 AAATGTTTCGAGAAAGTATCCAGTATGCCAGATGCCAAACAAAGACATGGTGTCCAGTCAAT 573
QY 481 GACGACTTCAGATTTTCAGGCATGATGGATACATGCTGATGCTTTCGAAGTACTT 540
DB 574 GACGACTTCAGATTTTCAGGCATGATGGATACATGCTGATGCTTTCGAAGTACTT 633
QY 541 GGCACCATCTCTCAAGTGGATCATCAATCAACTATCAAGGCTCCCGAGTACGTTGT 600
DB 634 GGCACCATCTCTCAAGTGGATCATCAATCAACTATCAAGGCTCCCGAGTACGTTGT 693
QY 601 GTGAAGAGTATCATTCGACAGGTCCTTCAAGGTTAGATTACTTACACAGTAAGTGCAG 660
DB 694 GTGAAGAGTATTCGACAGGTCCTTCAAGGTTAGATTACTTACACAGTAAGTGCAG 753
QY 661 ATCATTTTCATCTACATTAAGCCGAAATATCTTCATGTTGTGATGATGCATATG 720
DB 754 ATCATTTTCATCTACATTAAGCCGAAATATCTTCATGTTGTGATGATGCATATG 813

QY 721 AGAAGATGCGAGCTGAGGCCACTGAGTGGCAGAAACAGGAGTGTCTCTCTCTTCA-GG 779
DB 814 AGAAGATGCGAGCTGAGGCCACTGAGTGGCAGAAACAGGAGTGTCTCTCTCTTCA-RG 873
QY 780 GTCTGCGAGTGAATGCGCTCCACAGCAAGAACTATAGGAAATATCTAAACAAAAA 839
DB 874 GTMTTCAGTGAATGCGCTCCACAGCAAGAACTATAGGAAATATCTAAACAAAAA 933
QY 840 GAAAAAACTGAAAAAGAAACA 860
DB 934 RAAAAACYGAAAAAACA 954

RESULT 10
BU607396/c
LOCUS
DEFINITION
UI-CF-FNO-aeu-b-08-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
UI-CF-FNO-aeu-b-08-0-UI 3', mRNA sequence.
ACCESSION
BU607396
VERSION
BU607396.1 GI:23270671
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 735)
AUTHORS
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL
Genome Res. 6 (9), 791-806 (1996)
MEDLINE
97044477
PUBMED
8889548
COMMENT
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 686-735, >(TGG)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

Location/Qualifiers
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/db_xref="taxon:9606"
/clone="UI-CF-FNO-aeu-b-08-0-UI"
/tissue_type="Human lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/note="Organ: Lung; Vector: pYT73-Pac (Pharmacia) with a
modified polylinker; Site: EcoR I; Site_2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DU1) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
benito-soares@uiowa.edu
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

FEATURES
source

ORIGIN


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Query Match      34.8%; Score 730.4; DB 5; Length 735;
Best Local Similarity 99.5%; Pred. No. 1e-173; 4; Indels 0; Gaps 0;
Matches 731; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 112 CCACCGCCACCCACCCACCCACCCACCCCTTTGCCAGAGCCACCCACCCCGGAGCCAGAG 171
Db 735 CCACCGCCACCCACCCACCCACCCACCCCTTTGCCAGAGCCACCCACCCCGGAGCCAGAG 676

QY 172 GAGGAGATCTCTGGATCAGATGATGAGGACCAAGAGACCCCTGCGGACTACTGCAAGGT 231
Db 675 GAGGAGATCTCTGGATCAGATGATGAGGACCAAGAGACCCCTGCGGACTACTGCAAGGT 616

QY 232 GATATCATCCAGTAAATTTGAGACCTCTCAATGGCGGTATCATGCTATTAGAAAG 291
Db 615 GATATCATCCAGTAAATTTGAGACCTCTCAATGGCGGTATCATGCTATTAGAAAG 556

QY 292 CTTGGATGGGGCACCTTCTACTGCTGCTGCTGGATATGACGGGAAAGATTT 351
Db 555 CTTGGATGGGGCACCTTCTACTGCTGCTGCTGGATATGACGGGAAAGATTT 496

QY 352 GTTGCAATGAAGTTGTAAGTGGCCAGCATTTATACGAGACAGCCCTTGGATGAATA 411
Db 495 GTTGCAATGAAGTTGTAAGTGGCCAGCATTTATACGAGACAGCCCTTGGATGAATA 436

QY 412 AATGCTCAATGCTGTCGAGAAAGTATCCAGTGCACCCAGCAACCAAGACATGTTGTC 471
Db 435 AATGCTCAATGCTGTCGAGAAAGTATCCAGTGCACCCAGCAACCAAGACATGTTGTC 376

QY 472 CAGCTCATTTGACGACTTCAAGATTTTCAGGATGAATGGGATACATGCTGCAATGGTCTTC 531
Db 375 CAGCTCATTTGACGACTTCAAGATTTTCAGGATGAATGGGATACATGCTGCAATGGTCTTC 316

QY 532 GAAGTATTTGGCCACCATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGCCCTCCA 591
Db 315 GAAGTATTTGGCCACCATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGCCCTCCA 256

QY 592 GTACGTTGTTGAAGTATCATTCGACAGTCTTCAAGGTTAGATTTACTTACACAGT 651
Db 255 GTACGTTGTTGAAGTATCATTCGACAGTCTTCAAGGTTAGATTTACTTACACAGT 196

QY 652 AAGTGAAGATCATTTGATGATCAATAAAGCCGGAATAATCTTGATGTTGGATGAT 711
Db 195 AAGTGAAGATCATTTGATGATCAATAAAGCCGGAATAATCTTGATGTTGGATGAT 136

QY 712 GCATATGTGAGAAGATGCGAGCTGAGCCACTGAGTGGCAGAAAGCAGGTGCTCTCT 771
Db 135 GCATATGTGAGAAGATGCGAGCTGAGCCACTGAGTGGCAGAAAGCAGGTGCTCTCT 76

QY 772 CTTTCAAGGTTGTCAGTGTGAGTACGGCTCCACAGCAGAAACCTTATAGGAAATATCTAAA 831
Db 75 CTTTCAAGGTTGTCAGTGTGAGTACGGCTCCACAGCAGAAACCTTATAGGAAATATCTAAA 16

QY 832 AACAAAAAGAAAAA 846
Db 15 AACAAAAAGAAAAA 1

RESULT 11
CB242860/c
LOCUS
DEFINITION
UI-CF-FN0-sgb-e-16-0-UI.s1 UI-CF-FN0 Homo sapiens cDNA clone
CB242860
VERSION
CB242860.1 GI:28364504
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 728)
AUTHORS
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE
Normalization and subtraction: two approaches to facilitate gene
```

```
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.regen.com) or from Open Biosystems
(www.openbiosystems.com).
Seq primer: M13 FORWARD
POLYA=Yes.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FN0-sgb-e-16-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DH10B (Life Technologies) (Ti phage resistant)"
/clone_lib="UI-CF-FN0"
/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FN0 is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DUI) The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FN0
TAG_SEQ=GGCTGTAGGC"
ORIGIN
Query Match      34.5%; Score 723.2; DB 6; Length 728;
Best Local Similarity 99.6%; Pred. No. 6.7e-172;
Matches 725; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 119 CACCAACCACCCACCCACCCCTTTGCCAGAGCCACCCACCCCGGAGCCAGAGGAGA 178
Db 728 CACCAACCACCCACCCACCCCTTTGCCAGAGCCACCCACCCCGGAGCCAGAGGAGA 669

QY 179 TCCTGGATCAGATGATGAGGAGCAAGAGACCCCTGCGGACTACTGCAAAAGTGGATATC 238
Db 668 TCCTGGATCAGATGATGAGGAGCAAGAGACCCCTGCGGACTACTGCAAAAGTGGATATC 609

QY 239 ATCCAGTGAATTTGGAGACCTCTTCNATGGCGGTATCATGTTATTAGAAAGCTTGGAT 298
Db 608 ATCCAGTGAATTTGGAGACCTCTTCNATGGCGGTATCATGTTATTAGAAAGCTTGGAT 549

QY 299 GGGGGCCTTCTCTACTGCTGCTGCTGCGATATGACGGGAAAAAGATTTGTTGCCAA 358
Db 548 GGGGGCCTTCTCTACTGCTGCTGCTGCGATATGACGGGAAAAAGATTTGTTGCCAA 489

QY 359 TGAAAGTTGTAAAAAGTGCACAGCATTTATACGAGACAGCCCTTGGATGAAATAAATTCG 418
Db 488 TGAAAGTTGTAAAAAGTGCACAGCATTTATACGAGACAGCCCTTGGATGAAATAAATTCG 429

QY 419 TCAATATGTTTCGAGAAAGTATCCAGTGACCCCAACAAAGACATGGTGGTCCAGCTCA 478
Db 428 TCAATATGTTTCGAGAAAGTATCCAGTGACCCCAACAAAGACATGGTGGTCCAGCTCA 369

QY 479 TTGACGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTGTCATGGTCTTCGAAAGTAC 538
Db 368 TTGACGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTGTCATGGTCTTCGAAAGTAC 309
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QY 539 TTGGCCACCATTCTCTCAAGTGGATCATCAATCAACTATCAAGGCTCCAGTACGTT 598
Db 308 TTGGCCACCATTCTCTCAAGTGGATCATCAATCAACTATCAAGGCTCCAGTACGTT 249
QY 599 GTGTGAAGAGTATCATTTGACAGAGTCTTCAAGGTTAGATTACTTACACAGTAAAGTGA 658
Db 248 GTGTGAAGAGTATCATTTGACAGAGTCTTCAAGGTTAGATTACTTACACAGTAAAGTGA 189
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AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
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8889548
Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cdna
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FEATURES
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Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into p77T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
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site and the (dT)18 tail. The sequence tag for this
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Searched: 4300275 seqs, 2872944193 residues

Total number of hits satisfying chosen parameters: 8600550

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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3	2097	100.0	3253	17 US-10-799-676-1	Sequence 1, Appli
4	2028.6	96.7	3715	18 US-10-618-941-36	Sequence 36, Appli
5	2028.6	96.7	4698	14 US-10-198-846-10286	Sequence 10286, A
6	2023.8	96.5	3699	16 US-10-425-114-16424	Sequence 16424, A
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ALIGNMENTS

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; Sequence 1, Application US/09759359A
; Patent No. US20020094560A1
; GENERAL INFORMATION:
; APPLICANT: ASU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/09/759,359A
; CURRENT FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3253
; TYPE: DNA
; ORGANISM: Human
US-09-759-359A-1

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US-10-207-973-1

; Sequence 1. Application US/10207973

; Publication No. US20030175927A1.

; GENERAL INFORMATION:

; APPLICANT: ASU-THREIDEH, Jane et al

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001043

; CURRENT APPLICATION NUMBER: US/10/207,973

; CURRENT FILING DATE: 2002-07-31

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: FastSeq for Windows Version 4.0

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US-10-207-973-1

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DB 391 GGGCACTTCTCTACTGTCTGGCTGTCTGGGATATGACGGGAAAAAGATTGTTGCAATG 450
QY 361 AAAGTTGTAAGTCCCGAGCAATTTACGGAGACAGCCTTGGATGGAATAAATAATTTGCTC 420
DB 451 AAAGTTGTAAGTCCCGAGCAATTTACGGAGACAGCCTTGGATGGAATAAATAATTTGCTC 510
QY 421 AAATGTGTCGAGAAAGTGCATCCAGTGACCCAAACAAAGACATGCTGCTCAGCTCAT 480
DB 511 AAATGTGTCGAGAAAGTGCATCCAGTGACCCAAACAAAGACATGCTGCTCAGCTCAT 570
QY 481 GAGCACTTCAAGATTTTCAAGCATGAAATGGGATACATGCTCTGATGCTTTCGAAGTACT 540
DB 571 GAGCACTTCAAGATTTTCAAGCATGAAATGGGATACATGCTCTGATGCTTTCGAAGTACT 630
QY 541 GGCACCATCTCTCAAGTGGATCATCAAACTCAACTCAAGGCTCCAGTACGTTGT 600
DB 631 GGCACCATCTCTCAAGTGGATCATCAAACTCAACTCAAGGCTCCAGTACGTTGT 690
QY 601 GTGAGAGTATCATTCGACAGGCTCTTCAAGGTTAGATTACTTACACAGTAAGTGCAG 660
DB 691 GTGAGAGTATCATTCGACAGGCTCTTCAAGGTTAGATTACTTACACAGTAAGTGCAG 750
QY 661 ATCATTCATACGACATAAAGCCGAAAAATATCTTGATGTGTGGATGATGATATGTG 720
DB 751 ATCATTCATACGACATAAAGCCGAAAAATATCTTGATGTGTGGATGATGATATGTG 810
QY 721 AGAAGAAATGGCAGTCCAGGCTCTGAGTGGCAGAAAGCAGGCTCTCTCTCTCAGGG 780
DB 811 AGAAGAAATGGCAGTCCAGGCTCTGAGTGGCAGAAAGCAGGCTCTCTCTCTCAGGG 870
QY 781 TCTGAGTGTAGTACGGCTCCAGCAGCAACCTATAGGAAAAATATCTTAAAAACAAAAAG 840
DB 871 TCTGAGTGTAGTACGGCTCCAGCAGCAACCTATAGGAAAAATATCTTAAAAACAAAAAG 930
QY 841 AAAAACTCAAAAGAAAAAGAGAGCGCAGGCTGAGTTATTGGAGAGCGCTTCGAGGAG 900
DB 931 AAAAACTCAAAAGAAAAAGAGAGCGCAGGCTGAGTTATTGGAGAGCGCTTCGAGGAG 990
QY 901 ATAGAAAGAAATGGAGCGAGAGCTGAAAGGAAAAATATAGAGAAAAATCATCCTCAGCT 960
DB 991 ATAGAAAGAAATGGAGCGAGAGCTGAAAGGAAAAATATAGAGAAAAATCATCCTCAGCT 1050
QY 961 GCACCTTCCAAATGACAGGATGGCGAATATCTGCCAGAGGTGAACTAAAAACAACAGGA 1020

DB 1051 GCACCTTCCAAATGACAGGATGGCGAATACTGCCAGAGGTGAACTTAAAAACAACAGGA 1110
QY 1021 TTAGAGGAGGCGGCTGAGCAGAGACTGCAAAAGGCAAAATGGTGAAGCTGAGGACCAAGAA 1080
DB 1111 TTAGAGGAGGCGGCTGAGCAGAGACTGCAAAAGGCAAAATGGTGAAGCTGAGGACCAAGAA 1170
QY 1081 GAGAAAGAGATGCTGAGNAGAAAGAAACATTTGAAAAGATGAAGATGATCTAGATCAGGAA 1140
DB 1171 GAGAAAGAGATGCTGAGNAGAAAGAAACATTTGAAAAGATGAAGATGATCTAGATCAGGAA 1230
QY 1141 CTTGCGAAACATAGACCTACGTGGATAGAAATCACTTAAAAACCAATGGCCATATTGAGAAT 1200
DB 1231 CTTGCGAAACATAGACCTACGTGGATAGAAATCACTTAAAAACCAATGGCCATATTGAGAAT 1290
QY 1201 GGCCTATTCTCTACTGGAGCAGCAACTGGACGATGAAGATGATGAAGAAAGCTGCCCA 1260
DB 1291 GGCCTATTCTCTACTGGAGCAGCAACTGGACGATGAAGATGATGAAGAAAGCTGCCCA 1350
QY 1261 AATCCTGAGGATATATCTTCTGATGAGCCAAATGCAAGACGTGATACACATATAGCAGC 1320
DB 1351 AATCCTGAGGATATATCTTCTGATGAGCCAAATGCAAGACGTGATACACATATAGCAGC 1410
QY 1321 TCCATATGAACAAATCAATGGTGAATTTGCCAAATGGACGACATATAAAATTTCCGAGTCACAG 1380
DB 1411 TCCATATGAACAAATCAATGGTGAATTTGCCAAATGGACGACATATAAAATTTCCGAGTCACAG 1470
QY 1381 TTCCAGAGTTTTCACCTCGTTGTTCTCTGATCCTTAGAACCTGTGTGCGCTGCGCTCT 1440
DB 1471 TTCCAGAGTTTTCACCTCGTTGTTCTCTGATCCTTAGAACCTGTGTGCGCTGCGCTCT 1530
QY 1441 GTGCTTTCTGAGGATCACCCTTACTGAGCAAGAGGAGAGCAGTCCATCCCATGACAGA 1500
DB 1531 GTGCTTTCTGAGGATCACCCTTACTGAGCAAGAGGAGAGCAGTCCATCCCATGACAGA 1590
QY 1501 AGCAGAACGGTTTCAAGCTCAGTACTGGGATTTGCCAAAAAGCAAAAAACCCGGGAGCT 1560
DB 1591 AGCAGAACGGTTTCAAGCTCAGTACTGGGATTTGCCAAAAAGCAAAAAACCCGGGAGCT 1650
QY 1561 GACTTGTGTTGGTGAATCCCTCGGATCCGCGGAATGACAGATTAAGTGAAGTAAATTTGCT 1620
DB 1651 GACTTGTGTTGGTGAATCCCTCGGATCCGCGGAATGACAGATTAAGTGAAGTAAATTTGCT 1710
QY 1621 GACCTGGGAAATGCTTGTGGTGATATAACATTTACGGAAGACATCCAGAGCCTCAG 1680
DB 1711 GACCTGGGAAATGCTTGTGGTGATATAACATTTACGGAAGACATCCAGAGCCTCAG 1770
QY 1681 TACCGCTCCATAGAGGTTTAAATAGAGCGGGGTACAGCACCCCTCGCGACATCTCGAGC 1740
DB 1771 TACCGCTCCATAGAGGTTTAAATAGAGCGGGGTACAGCACCCCTCGCGACATCTCGAGC 1830
QY 1741 ACGGGCTGTATGGCATTTGAGCTGGCAACGGGAGATTTATTTGTTGAACCAATTTCTGGG 1800
DB 1831 ACGGGCTGTATGGCATTTGAGCTGGCAACGGGAGATTTATTTGTTGAACCAATTTCTGGG 1890
QY 1801 GAAGACTATTTCAGAGACGAAGACACATAGGCCACATCATAGAGCTGTAGCAGTATT 1860
DB 1891 GAAGACTATTTCAGAGACGAAGACACATAGGCCACATCATAGAGCTGTAGCAGTATT 1950
QY 1861 CCAAGGCACTTTGCTCTATCTGAAAAATTTCTCGGAAATTTCTCAATCGAGAGGAGAA 1920
DB 1951 CCAAGGCACTTTGCTCTATCTGAAAAATTTCTCGGAAATTTCTCAATCGAGAGGAGAA 2010
QY 1921 CTGCGACACATCAACAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGGAAAAAGTAT 1980
DB 2011 CTGCGACACATCAACAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGGAAAAAGTAT 2070
QY 1981 GCGTGGCCCCATGAAGATGCTGCACAGTTTACAGATTTCTGATCCCGATGTTAGAAATG 2040
DB 2071 GCGTGGCCCCATGAAGATGCTGCACAGTTTACAGATTTCTGATCCCGATGTTAGAAATG 2130
QY 2041 GTTCCAGAAAAACGAGCCTCAGCTGGCAATCGCTTCGCACTCTTGTGTAATCT 2097

Db 2131 GTTCCAGAAAACGAGCCTCAGCTGGCGAATGCCCTTGGCATCCTTGGTGAATTC 2187

RESULT 3
US-10-799-676-1
; Sequence 1, Application US/10799676
; Publication No. US20040157297A1
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001043DIV II
; CURRENT APPLICATION NUMBER: US/10/799,676
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: 10/207,973
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 09/759,359
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3253
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-799-676-1

Query Match 100.0%; Score 2097; DB 17; Length 3253;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTCCCGAAAGTGTGCGCCATTACAGGCCGAAAGCGGAGCGCCGAAAGAGAGAAA 60
Db 91 ATGAGCTCCCGAAAGTGTGCGCCATTACAGGCCGAAAGCGGAGCGCCGAAAGAGAGAAA 150
QY 61 CATCCGAAAAAGCCGGAGCCTCAACAGAAAAGTCTCTTTAGTTCTCTCTCCACCGCCA 120
Db 151 CATCCGAAAAAGCCGGAGCCTCAACAGAAAAGTCTCTTTAGTTCTCTCTCCACCGCCA 210
QY 121 CCACACACACCGCCGCTTTGCCAGACCCACACCCCGGAGCCGAGAGGAGATC 180
Db 211 CCACACACACCGCCGCTTTGCCAGACCCACACCCCGGAGCCGAGAGGAGATC 270
QY 181 CTGGGATCAGATGATGAGGAGCAAGAGACCTTGGCGACTACTGCAAAAGGTGGATATCAT 240
Db 271 CTGGGATCAGATGATGAGGAGCAAGAGACCTTGGCGACTACTGCAAAAGGTGGATATCAT 330
QY 241 CCAGTGAAAATTGGAGACCTTCAATGGCCGGTATCATGTTATTAGAAAAGCTTGGATGG 300
Db 331 CCAGTGAAAATTGGAGACCTTCAATGGCCGGTATCATGTTATTAGAAAAGCTTGGATGG 390
QY 301 GGCGACTTCTTACTGTCTGGCTGTGCTGGGATATGCGGGGAAAGATTGTTGCAATG 360
Db 391 GGCGACTTCTTACTGTCTGGCTGTGCTGGGATATGCGGGGAAAGATTGTTGCAATG 450
QY 361 AAAAGTTGTAAGTGTCCAGCATTTACGGAGACAGCCCTTGGATGAAAATAAAATGCTC 420
Db 451 AAAAGTTGTAAGTGTCCAGCATTTACGGAGACAGCCCTTGGATGAAAATAAAATGCTC 510
QY 421 AAATGTTTCGAAAAGTATCCAGTGCACCCCAAAAGACATGCTGCTCCAGCTCAT 480
Db 511 AAATGTTTCGAAAAGTATCCAGTGCACCCCAAAAGACATGCTGCTCCAGCTCAT 570
QY 481 GAGCACTTCAAGATTTTCAGGCATGAATGGATACATGCTGATGCTCTTCAAGTACT 540
Db 571 GAGCACTTCAAGATTTTCAGGCATGAATGGATACATGCTGATGCTCTTCAAGTACT 630
QY 541 GGCCACCATCTCTCAAGTGGATCATCAAACTCAACTCAAGGCCCTCCAGTACGTTGT 600
Db 631 GGCCACCATCTCTCAAGTGGATCATCAAACTCAACTCAAGGCCCTCCAGTACGTTGT 690
QY 601 GTGAGAGTATCATTTCGACAGGTCCTTCAAGGTTAGATTACTTACAGATGATGCAAG 660

Db 691 GTGAAGAGTATCATTCGACAGGTCCTTTCAAGGGTTAGATTACTTTACAGATAAGTCAAG 750
QY 661 ATCAATTCATCTACTGACATAAAAGCCGAAAAATATCTTTGATGTGTGTGGATGATGATATGTG 720
Db 751 ATCAATTCATCTGACATAAAAGCCGAAAAATATCTTTGATGTGTGTGGATGATGATATGTG 810
QY 721 AGAAGAATGGCAGCTGAGGCCACTGAGTGGCAGAAAAGCAGGTGCTCTCTCTCTTCAGGG 780
Db 811 AGAAGAATGGCAGCTGAGGCCACTGAGTGGCAGAAAAGCAGGTGCTCTCTCTCTTCAGGG 870
QY 781 TCTCAGTGTAGTACGGCTCCACAGCAGAAAACCTATAGAAAAATATCTAAAAACAAAAAG 840
Db 871 TCTCAGTGTAGTACGGCTCCACAGCAGAAAACCTATAGAAAAATATCTAAAAACAAAAAG 930
QY 841 AAAAAACCTGAAAAAGAAACAGAGAGGCGAGCTCAGTTATTGGAGAAAGCGCTCGAGAG 900
Db 931 AAAAAACCTGAAAAAGAAACAGAGAGGCGAGCTCAGTTATTGGAGAAAGCGCTCGAGAG 990
QY 901 ATAGAAGAATTTGGAGCGAGAAAGCTGAAAGGAAAAATAATAGAAAAACATCACCTCAGCT 960
Db 991 ATAGAAGAATTTGGAGCGAGAAAGCTGAAAGGAAAAATAATAGAAAAACATCACCTCAGCT 1050
QY 961 GCACCTTCCAAATGACCGAGGTGCGAATACCTGCCAGAGGTGAAACTAAAAACAAACAGGA 1020
Db 1051 GCACCTTCCAAATGACCGAGGTGCGAATACCTGCCAGAGGTGAAACTAAAAACAAACAGGA 1110
QY 1021 TTAGAGGAGCGGCTGAGGCGAGAGACTGCCAAGGACCAATGTGTAAGCTGAGGACCAAGAA 1080
Db 1111 TTAGAGGAGCGGCTGAGGCGAGAGACTGCCAAGGACCAATGTGTAAGCTGAGGACCAAGAA 1170
QY 1081 GAGAAAGAATGCTGAGAAAAAACAATTGAAAAAGATGAAGATGATGTAGATCAGGAA 1140
Db 1171 GAGAAAGAATGCTGAGAAAAAACAATTGAAAAAGATGAAGATGATGTAGATCAGGAA 1230
QY 1141 CTTGCGAACATAGACCTTACCTGCGATGAAATCACTTAAACCAATGGCCATATTGAGAA 1200
Db 1231 CTTGCGAACATAGACCTTACCTGCGATGAAATCACTTAAACCAATGGCCATATTGAGAA 1290
QY 1201 GGCCCATCTCTCACTGGAGCAGCAACTGGACGATGAAGATGATGAAGAGAGCTGCCCA 1260
Db 1291 GGCCCATCTCTCACTGGAGCAGCAACTGGACGATGAAGATGATGAAGAGAGCTGCCCA 1350
QY 1261 AATCTCTGAGGAATATATCTTTGATGAGCCAAATGCGAAGATGATTAACATATAGCAGC 1320
Db 1351 AATCTCTGAGGAATATATCTTTGATGAGCCAAATGCGAAGATGATTAACATATAGCAGC 1410
QY 1321 TCCTATGAACAATTCATGTTGAAATGCAATGGAACACATATAAATCCCGAGTCACAG 1380
Db 1411 TCCTATGAACAATTCATGTTGAAATGCAATGGAACACATATAAATCCCGAGTCACAG 1470
QY 1381 TTCCAGAGTTTTCACCTCGTTGTTCTCTGGATCTTTAGAACCTGTGGCTGCGGCTCT 1440
Db 1471 TTCCAGAGTTTTCACCTCGTTGTTCTCTGGATCTTTAGAACCTGTGGCTGCGGCTCT 1530
QY 1441 GTGCTTCTGAGGATCACCATTACTGAGCAAGGAGAGAGCAGTCCATCCCATCAGAGA 1500
Db 1531 GTGCTTCTGAGGATCACCATTACTGAGCAAGGAGAGAGCAGTCCATCCCATCAGAGA 1590
QY 1501 AGCAGAACGGTTTCAGCCTCCAGTCTGCGGATTTGCCAAAAAGCAAAAAACCCGGGAGCT 1560
Db 1591 AGCAGAACGGTTTCAGCCTCCAGTCTGCGGATTTGCCAAAAAGCAAAAAACCCGGGAGCT 1650
QY 1561 GACTTGTGTTGAATCCCTCGATCCGCGGAATGAGATAAATAATAGAGTAAAAATTCCT 1620
Db 1651 GACTTGTGTTGAATCCCTCGATCCGCGGAATGAGATAAATAATAGAGTAAAAATTCCT 1710
QY 1621 GACCTGGGAAATCTTTGTTGGTGATATAACATTTACGGAAGACATCCAGACGCTCAG 1680
Db 1711 GACCTGGGAAATCTTTGTTGGTGATATAACATTTACGGAAGACATCCAGACGCTCAG 1770
QY 1681 TACCCTCTCCATAGAGTTTAAATAGGAGCGGGGTACAGCACCCCTGCGGACATCTGGAGC 1740
Db 1771 TACCCTCTCCATAGAGTTTAAATAGGAGCGGGGTACAGCACCCCTGCGGACATCTGGAGC 1830

QY 1741 ACGCGCTGTATGCGCATTTGAGCTGGCAACGGAGAGATTATTTGTTTGAACACATTTCTGGG 1800
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Db 1831 ACGCGCTGTATGCGCATTTGAGCTGGCAACGGAGAGATTATTTGTTTGAACACATTTCTGGG 1890
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QY 1801 GAAGACTATTCCAGAGACGAAGAACACATAGAGCCACATCATAGAGCTGCTAGGAGATTT 1860
|||||
Db 1891 GAAGACTATTCCAGAGACGAAGAACACATAGAGCCACATCATAGAGCTGCTAGGAGATTT 1950
|||||
QY 1861 CMAAGCACTTTGCTCTATCTATCTGGAATAATTTCTCGGGAAATTTCTCAATCGAGAGAGAA 1920
|||||
Db 1951 CMAAGCACTTTGCTCTATCTATCTGGAATAATTTCTCGGGAAATTTCTCAATCGAGAGAGAA 2010
|||||
QY 1921 CTGCGACACATACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGGAAAGATAT 1980
|||||
Db 2011 CTGCGACACATACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGGAAAGATAT 2070
|||||
QY 1981 GGTGCGCCCATGAAGATGCTGCACAGTTTACAGATTTCTGATCCCGATGTTAGAAATG 2040
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Db 2071 GGTGCGCCCATGAAGATGCTGCACAGTTTACAGATTTCTGATCCCGATGTTAGAAATG 2130
|||||
QY 2041 GTTCCAGAAACAGAGCCTCAGCTGGCGAATGCTTCCGATCCTTGGTGTGAATTC 2097
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Db 2131 GTTCCAGAAACAGAGCCTCAGCTGGCGAATGCTTCCGATCCTTGGTGTGAATTC 2187
|||||

RESULT 4

US-10-618-941-36
; Sequence 36, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:

; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; PRIORITY FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 3715
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-618-941-36

Query Match 96.7%; Score 2028.6; DB 18; Length 3715;

Best Local Similarity 99.8%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Matches 2031; Conservative 0;

QY 63 TCCGAAAAAGCCGGAGCCTCAACAGAAAGCTCTTTAGTTCTCTCTCTCCACCGCCACC 122
|||||
Db 208 TTCAGAAAGCCGGAGCCTCAACAGAAAGCTCTTTAGTTCTCTCTCTCCACCGCCACC 267
|||||
QY 123 ACCACCAACCGCCACCTTTGCGAGACCCCAACACCCCGAGCCAGAGAGAGATCCT 182
|||||
Db 268 ACCACCAACCGCCACCTTTGCGAGACCCCAACACCCCGAGCCAGAGAGAGATCCT 327
|||||
QY 183 GGGATCAGATGATGAGGACAGAGACCTTCGGGACTACTGCAAGGTTGGATATCATCC 242
|||||
Db 328 GGGATCAGATGATGAGGACAGAGACCTTCGGGACTACTGCAAGGTTGGATATCATCC 387
|||||
QY 243 AGTGAATAATGGAGACTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 302
|||||
Db 388 AGTGAATAATGGAGACTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 447
|||||
QY 303 GCACTTCTACTGCTGCTGCTGGATATGCAAGGGAAGATTTGTTGCAATGAA 362
|||||
Db 448 GCACTTCTACTGCTGCTGCTGGATATGCAAGGGAAGATTTGTTGCAATGAA 507
|||||
QY 363 AGTTGTAANAAGTCCAGCATTTATACGGAGACAGCCTTGGATGAATAAATTTGCTCAA 422
|||||

Db 508 AGTTGTAANAAGTCCAGCATTTATACGGAGACAGCCTTGGATGAATAAATTTGCTCAA 567
|||||
QY 423 ATGTGTTCCGAAAGATGATCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATTTGA 482
|||||
Db 568 ATGTGTTCCGAAAGATGATCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATTTGA 627
|||||
QY 483 CGACATTCAGATTTCCAGGCATGAATGGGATACATGTCGTCATGGTCTTCCGAGTACTTGG 542
|||||
Db 628 CGACATTCAGATTTCCAGGCATGAATGGGATACATGTCGTCATGGTCTTCCGAGTACTTGG 687
|||||
QY 543 CCACCATCTCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCAGTACTTGTGT 602
|||||
Db 688 CCACCATCTCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCAGTACTTGTGT 747
|||||
QY 603 GAAGAGTATCATTTCCAGAGTCTCTTCAAGGGTTAGATTACTTACACAGTAAGTGCAGAT 662
|||||
Db 748 GAAGAGTATCATTTCCAGAGTCTCTTCAAGGGTTAGATTACTTACACAGTAAGTGCAGAT 807
|||||
QY 663 CATTCATCTACTGACATAAAGCCGGAATAATCTTTGATGTGTGTGGATGATGCATATGTAG 722
|||||
Db 808 CATTCATCTACTGACATAAAGCCGGAATAATCTTTGATGTGTGTGGATGATGCATATGTAG 867
|||||
QY 723 AAGAAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCAGGGTC 782
|||||
Db 868 AAGAAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCAGGGTC 927
|||||
QY 783 TGCAGTGTACGGTCTCCACAGCAGAAACCTTAGGAAAAATATCTTAAAAACAAAAAGAA 842
|||||
Db 928 TGCAGTGTACGGTCTCCACAGCAGAAACCTTAGGAAAAATATCTTAAAAACAAAAAGAA 987
|||||
QY 843 AAAAAGTGTGAGCAGAGAGAGCAGGTGAGTTATTTGGAGAGCGGCTGCAGAGAT 902
|||||
Db 988 AAAAAGTGTGAGCAGAGAGAGCAGGTGAGTTATTTGGAGAGCGGCTGCAGAGAT 1047
|||||
QY 903 AGAAGAAATTTGGAGCCAGAGAGCTGAAAGGAAAAATATAGAGAGAAACATCACCTCAGCTGC 962
|||||
Db 1048 AGAAGAAATTTGGAGCCAGAGAGCTGAAAGGAAAAATATAGAGAGAAACATCACCTCAGCTGC 1107
|||||
QY 963 ACCTTTCCAATGATCCAGGATGGCGAATATCTGCCAGAGGTGAAATCTAAAAACAAACAGAT 1022
|||||
Db 1108 ACCTTTCCAATGATCCAGGATGGCGAATATCTGCCAGAGGTGAAATCTAAAAACAAACAGAT 1167
|||||
QY 1023 AGAGAGCGGCTGAGGCGAGAGACTGCAAGAGACAAATGCTGAAGCTGAGAGCAGAGAA 1082
|||||
Db 1168 AGAGAGCGGCTGAGGCGAGAGACTGCAAGAGCAATGCTGAAGCTGAGAGCAGAGAA 1227
|||||
QY 1083 GAAAGAGATGCTGAGAAAGAAAAACATTCGAAAAAGATGAAGATGATGTAGATCAGGAACT 1142
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Db 1228 GAAAGAGATGCTGAGAAAGAAAAACATTCGAAAAAGATGAAGATGATGTAGATCAGGAACT 1287
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QY 1143 TCCGAACATAGACCTTACGTGGATAGAATCACCTAAAAACCAATGGCCATATTGAGAAATGG 1202
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Db 1288 TCCGAACATAGACCTTACGTGGATAGAATCACCTAAAAACCAATGGCCATATTGAGAAATGG 1347
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QY 1203 CCATTTCTCAGTGGAGAGCAACCTGGAAGATGAAGATGATGAAGAGAGATGAGAGAGATGAG 1262
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Db 1348 CCATTTCTCAGTGGAGAGCAACCTGGACGATGAAGATGATGAAGAGAGATGAGAGAGATGAG 1407
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QY 1263 TCCAGGAAATATATCTTTGATGAGCCAAATGCAAGAGATGATTAACATATAGCAGCTC 1322
|||||
Db 1408 TCCAGGAAATATATCTTTGATGAGCCAAATGCAAGAGATGATTAACATATAGCAGCTC 1467
|||||
QY 1323 CTATGAAACAAATTTCAATGGTGAATTTGCCAAATGGACACATAAATTTCCGAGTTCACAGTT 1382
|||||
Db 1468 CTATGAAACAAATTTCAATGGTGAATTTGCCAAATGGACACATAAATTTCCGAGTTCACAGTT 1527
|||||
QY 1383 CCCAGAGTTTCCACTCGTGTCTCTGAGTCTTTAGAAACCTGTGGCCTGCGGCTCTGT 1442
|||||
Db 1528 CCCAGAGTTTCCACTCGTGTCTCTGAGTCTTTAGAAACCTGTGGCCTGCGGCTCTGT 1587
|||||
QY 1443 GCTTTCTGAGGATCACCACTTACTGAGCAAGGAGAGAGCTCCATCCCATGACAGAAAG 1502
|||||

Db 1588 GCTTCTCAGGGATCACCACTTACTGTAGCAAGAGGAGGAGCTCCATCCCATGACAGAAG 1647
QY 1503 CAGAACGGTTTCAGCTCAGTACTGCGGATTTGCGCAAAAGCAAAACCCGGGAGCTGA 1562
Db 1648 CAGAACGGTTTCAGCTCAGTACTGCGGATTTGCGCAAAAGCAAAACCCGGGAGCTGA 1707
QY 1563 CTGTGTTGTAATCCCTTGGATCCGCGAATGCGAATGAGATAAAATAGAGTAAAAATTTGCTGA 1622
Db 1708 CTGTGTTGTAATCCCTTGGATCCGCGAATGCGAATGAGATAAAATAGAGTAAAAATTTGCTGA 1767
QY 1623 CTTGGGAAATGCTTGTGGTGATCAATAAATGAGTAAAAATTTGCTGA 1682
Db 1768 CTTGGGAAATGCTTGTGGTGATCAATAAATGAGTAAAAATTTGCTGA 1827
QY 1683 CCGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTGCGGACATCTGGAGCAC 1742
Db 1828 CCGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTGCGGACATCTGGAGCAC 1887
QY 1743 GCGGTGATGGCATTTGAGCTGGCAACGGGAGATTATTTGTTGAACACATTTCTGGGGA 1802
Db 1888 GCGGTGATGGCATTTGAGCTGGCAACGGGAGATTATTTGTTGAACACATTTCTGGGGA 1947
QY 1803 AGACTATTCAGAGACGAGAACACATAGCCACATCATAGAGCTGTAGGAGTATTC 1862
Db 1948 AGACTATTCAGAGACGAGAACACATAGCCACATCATAGAGCTGTAGGAGTATTC 2007
QY 1863 AAGGCATTTGCTCTATCTGGAATATTTCTGGGAATTTCTCAATCGCAGAGGAACT 1922
Db 2008 AAGGCATTTGCTCTATCTGGAATATTTCTGGGAATTTCTCAATCGCAGAGGAACT 2067
QY 1923 GCGACATCACCAAGCTGAAGCCCTGGAGCCCTTTGATGATCTTTGTTGAAAAAGTATGG 1982
Db 2068 GCGACATCACCAAGCTGAAGCCCTGGAGCCCTTTGATGATCTTTGTTGAAAAAGTATGG 2127
QY 1983 CTGGCCCATGAGATGCTGCAAGTTTACAGATTTCTCGATCCCGATGTTAGAAATGGT 2042
Db 2128 CTGGCCCATGAGATGCTGCAAGTTTACAGATTTCTCGATCCCGATGTTAGAAATGGT 2187
QY 2043 TCCGAAAAACGAGCTCAGCTGGGAAATGCTTGGCAATCTTGGTTGAATTC 2097
Db 2188 TCCGAAAAACGAGCTCAGCTGGGAAATGCTTGGCAATCTTGGTTGAATTC 2242

RESULT 5

US-10-198-846-10286
; Sequence 10286, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10286
; LENGTH: 4698
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-10286

Query Match 96.7%; Score 2028.6; DB 14; Length 4698;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2031; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 63 TCCGAAAAACGCGAGCTCAACAGAAAGCTCTTTAGTTCTCTCTCCCTCCAGCCACC 122

Db 254 TTCAAGAAAGCCGAGAGCTCAACAGAAAGCTCTCTTTAGTTCTCTCTCCAGCCGACC 313
QY 123 ACCACACACACCCGAGCTTTGCGAGACCCACACCCCGGAGCCAGAGGAGAGATCCT 182
Db 314 ACCACACACACCCGAGCTTTGCGAGACCCACACCCCGGAGCCAGAGGAGAGATCCT 373
QY 183 GGGATCAGATGATGAGGAGCAAGAGGACCTTGGGACTACTGCAAAAGGTGATATCATCC 242
Db 374 GGGATCAGATGATGAGGAGCAAGAGGACCTTGGGACTACTGCAAAAGGTGATATCATCC 433
QY 243 AGTGAAATTTGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTCGATGGGG 302
Db 434 AGTGAAATTTGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTCGATGGGG 493
QY 303 GCATCTCTACTGCTGCTGGGATATGCGAGGGAAGAAAGATTGTTTCAATGAA 362
Db 494 GCATCTCTACTGCTGCTGGGATATGCGAGGGAAGAAAGATTGTTTCAATGAA 553
QY 363 AGTTGTAAAAAGTCCCGAGCATTTATACGAGAGACAGCTTGGATGAATAAATTTGCTCAA 422
Db 554 AGTTGTAAAAAGTCCCGAGCATTTATACGAGAGACAGCTTGGATGAATAAATTTGCTCAA 613
QY 423 ATGTGTTGAGAAAGTATCCAGTGCACCAACAAAGACATGCTGCTCCAGCTCATTTGA 482
Db 614 ATGTGTTGAGAAAGTATCCAGTGCACCAACAAAGACATGCTGCTCCAGCTCATTTGA 673
QY 483 CGACTTCAAGATTTTCAAGGATGATGCTGATGCTGCTGATGCTTTCGAAGTACTTGG 542
Db 674 CGACTTCAAGATTTTCAAGGATGATGCTGATGCTGCTGATGCTTTCGAAGTACTTGG 733
QY 543 CCACCATCTCTCAAGTGGATCATCAATCAACTCAAGGCTCCAGCTACGTTGTTGT 602
Db 734 CCACCATCTCTCAAGTGGATCATCAATCAACTCAAGGCTCCAGCTACGTTGTTGT 793
QY 603 GAAAGTATCATTTGCGAGGCTCTTCAAGGTTAGATTACTTACACAGTAAGTCAAGAT 662
Db 794 GAAAGTATCATTTGCGAGGCTCTTCAAGGTTAGATTACTTACACAGTAAGTCAAGAT 853
QY 663 CATTCATACCTGACATAAAGCCGGAATAATCTTGTGATGCTGTTGGATGATGATGTGAG 722
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QY 723 AAGAAATGCGAGCTGAGGCTGAGTGGCAGAAAGAGGCTCTCTCTCTCCAGGCTC 782
Db 914 AAGAAATGCGAGCTGAGGCTGAGTGGCAGAAAGAGGCTCTCTCTCTCCAGGCTC 973
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QY 1023 AGAGGAGCGGCTGAGGAGAGCTGCAAGAGCAATGCTGAGCTGAGGACCGAGAGA 1082
Db 1214 AGAGGAGCGGCTGAGGAGAGCTGCAAGAGCAATGCTGAGCTGAGGACCGAGAGA 1273
QY 1083 GAAAGAGATGCTGAGAAAGAAACATTTGAAAGATGAAGATGATGTAGATCAGGAACT 1142
Db 1274 GAAAGAGATGCTGAGAAAGAAACATTTGAAAGATGAAGATGATGTAGATCAGGAACT 1333
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Db 1334 TCGAACATAGACCCCTACGTGGATAGAAATCACCTAAAAACCAATGGCCATATTGAGAATGG 1393
Qy 1203 CCATTTCTCACTGGAGCAACTGCAAGATGAAGATGATGAAGAAGACTGCCCAA 1262
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Qy 1503 CAGAACGGTTTCCAGCTTCCAGTACTGGGATTTGCCAAAGCAAAACCCGGGACGTGA 1562
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Qy 1563 CTTGTTGGTGAATCCCTGATCCCGGGAATGAGATAAATTTAGAGTAAATTTGCTGA 1622
Db 1754 CTTGTTGGTGAATCCCTGATCCCGGGAATGAGATAAATTTAGAGTAAATTTGCTGA 1813
Qy 1623 CTTGGGAATGCTTTGTTGGTGCATAAACACTTCCGGAAGACATCCAGACGGTCAGTA 1682
Db 1814 CTTGGGAATGCTTTGTTGGTGCATAAACACTTCCGGAAGACATCCAGACGGTCAGTA 1873
Qy 1683 CCGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTCGGACATCTGGAGCAC 1742
Db 1874 CCGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTCGGACATCTGGAGCAC 1933
Qy 1743 GCGTGTATGGCAATTTGAGCTGGCAACGGGAGATTTTGTGTAACCAATTTCTGGGA 1802
Db 1934 GCGTGTATGGCAATTTGAGCTGGCAACGGGAGATTTTGTGTAACCAATTTCTGGGA 1993
Qy 1803 AGACTATCCAGAGCGAAGACACATAGCCACATAGAGCTGCTAGGAGTATCC 1862
Db 1994 AGACTATCCAGAGCGAAGACACATAGCCACATAGAGCTGCTAGGAGTATCC 2053
Qy 1863 AAGGCATTTGCTCTATCTGGAATAATTTCTGGGAATTTCTCAATCGCAGAGGAAC 1922
Db 2054 AAGGCATTTGCTCTATCTGGAATAATTTCTGGGAATTTCTCAATCGCAGAGGAAC 2113
Qy 1923 GCGACATCACCAAGCTGAAGCCCTGGAGCCTTTGTATGATCTTTGTGGAAGATG 1982
Db 2114 GCGACATCACCAAGCTGAAGCCCTGGAGCCTTTGTATGATCTTTGTGGAAGATG 2173
Qy 1983 CTGGCCCATGAGATGCTGCAGATTACAGATTTCTGATCCCGATGTTAGAAATG 2042
Db 2174 CTGGCCCATGAGATGCTGCAGATTACAGATTTCTGATCCCGATGTTAGAAATG 2233
Qy 2043 TCCAGAAAAACGAGCTCAGCTGGGGAATGCTTGGGCATCTTGGTTCGAATTC 2097
Db 2234 TCCAGAAAAACGAGCTCAGCTGGGGAATGCTTGGGCATCTTGGTTCGAATTC 2288

RESULT 6

US-10-425-114-16424
; Sequence 16424, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 16424
; LENGTH: 3699
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3063-134-E5_FLI
US-10-425-114-16424

Query Match 96.5%; Score 2023.8; DB 16; Length 3699;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 2028; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 63 TCGAAAAAGCCGGAGCCTCAACAGAAAGCTCTTTAGTTCTCTCTCCACCCGCCACC 122
Db 199 TTCAGAAAAGCCGGAGCCTCAACAGAAAGCTCTTTAGTTCTCTCTCCACCCGCCACC 258
Qy 123 ACCACCACCCAGCCACCTTTGCCAGACCCACACCCCGGAGCCAGAGGAGATCCT 182
Db 259 ACCACACACCCAGCCACCTTTGCCAGACCCACACCCCGGAGCCAGAGGAGATCCT 318
Qy 183 GGGATCAGATGATGAGGACCAAGAGACCTCTCGGACTACTGCAAGGTGGATCATCC 242
Db 319 GGGATCAGATGATGAGGACCAAGAGACCTCTCGGACTACTGCAAGGTGGATCATCC 378
Qy 243 AGTGAATTTGAGACCTCTTCAATGGCCGGTATCATTTATTAGAAAGCTTGGATGGGG 302
Db 379 AGTGAATTTGAGACCTCTTCAATGGCCGGTATCATTTATTAGAAAGCTTGGATGGGG 438
Qy 303 GCACCTTCTACTGTCTGCTGTGGATGATGAGGGGAAAGATTTGTTGCAATGAA 362
Db 439 GCACCTTCTACTGTCTGCTGTGGATGATGAGGGGAAAGATTTGTTGCAATGAA 498
Qy 363 AGTTGTAAAAAGTGCCAGCATTATACGGAGACAGCCTTTGGATGAAATAAATTTGCTCAA 422
Db 499 AGTTGTAAAAAGTGCCAGCATTATACGGAGACAGCCTTTGGATGAAATAAATTTGCTCAA 558
Qy 423 ATGTGTTGAGAAAGTATCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATTTGA 482
Db 559 ATGTGTTGAGAAAGTATCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATTTGA 618
Qy 483 CGACTTCAAGATTTTCAAGCATGAATGGGATACATGCTGATGCTTCCGAGTACTTGG 542
Db 619 CGACTTCAAGATTTTCAAGCATGAATGGGATACATGCTGATGCTTCCGAGTACTTGG 678
Qy 543 CCACCATCTCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCAGTACTGTTGT 602
Db 679 CCACCATCTCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCAGTACTGTTGT 738
Qy 603 GAAGAGTATCATTCGACAGGTCTTCAAGGGTTAGATTACTTACACAGTAAGTCAAGAT 662
Db 739 GAAGAGTATCATTCGACAGGTCTTCAAGGGTTAGATTACTTACACAGTAAGTCAAGAT 798
Qy 663 CATTCATCTGACATAAAGCCGGAATAATCTTGTGTTGGATGATGATATGTGAG 722
Db 799 CATTCATCTGACATAAAGCCGGAATAATCTTGTGTTGGATGATGATATGTGAG 858
Qy 723 AAGAATGGCAGCTGAGGCCCTAGTGGCAGAAAGCAGGTGCTCTCTCTCTCCAGGGTC 782
Db 859 AAGAATGGCAGCTGAGGCCCTAGTGGCAGAAAGCAGGTGCTCTCTCTCTCCAGGGTC 918
Qy 783 TGCAGTGAAGTACGGCTCCACAGCAAAACCTATAGGAAAAATATCTTAAAAACAAAAAGAA 842
Db 919 TGCAGTGAAGTACGGCTCCACAGCAAAACCTATAGGAAAAATATCTTAAAAACAAAAAGAA 978
Qy 843 AAAAAGTGAAGTACGGCTCCACAGCAAAACCTATAGGAAAAATATCTTAAAAACAAAAAGAA 902

Db 697 CCACCATCTCTCAAGTGGATCATCAAAATCCAATATCAAGGCCTCCACGTAGCTTGTGT 756
Qy 603 GAAGAGTATCATTCGACAGGTCTTCAAGGGTAGATTACTTACACAGTAAGTGCAGAT 662
Db 757 GAAGAGTATCATTCGACAGGTCTTCAAGGGTAGATTACTTACACAGTAAGTGCAGAT 816
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Qy 723 AAGATGGCAGCTGAGGCCACCTGAGTGGCAGAAAGCAGGTGCTCTCTTCCAGGGTTC 782
Db 877 AAGATGGCAGCTGAGC---CTGAGTGGCAGAAAGCAGGTGCTCTCTCTTCCAGGGTTC 933
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Db 1414 TCTGAGGAATATAATCTTTGATGAGCCAAATGAGAAAGTGAATACACATATAGCAGCTC 1473
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Db 1474 CTATGAAACATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1533
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Db 1654 CAGAACGGTTTTCAGCTCAGTACCTGGGATTTGCAAAAGCAAAACCCCGGCGAGCTGA 1713
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Db 1714 CTGTGTGTGATCCCTCGATCCCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1773
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Db 1774 CTGTGTGTGATCCCTCGATCCCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1833

Qy 1683 CCGCTCCATAGAGGTTTTTAATAGGAGCGGGTACACAGACCCCTCGGACATCTGGAGCAC 1742
Db 1834 CCGCTCCATAGAGGTTTTTAATAGGAGCGGGTACACAGACCCCTCGGAGCATCTGGAGCAC 1893
Qy 1743 GCGGTGTATGGCATTTGAGCTGGCAACGGGAGATTATTTGTTTGAACCAACATTTCTGGGA 1802
Db 1894 GCGGTGTATGGCATTTGAGCTGGCAACGGGAGATTATTTGTTTGAACCAACATTTCTGGGA 1953
Qy 1803 AGACTATTCCAGAGAGAGAACCAATAGCCCCACATCATATAGAGCTGCTAGGAGATATTC 1862
Db 1954 AGACTATTCCAGAGAGAGAACCAATAGCCCCACATCATATAGAGCTGCTAGGAGATATTC 2013
Qy 1863 AAGGACATTTGCTCTATCTGGAATAATTTCTCGGAAATTTCTCGGAAATTTCTCGGAAATTTCT 1922
Db 2014 AAGGACATTTGCTCTATCTGGAATAATTTCTCGGAAATTTCTCGGAAATTTCTCGGAAATTTCT 2073
Qy 1923 GCGACACATCACCAAGCTGAAGCCCTGGAGCCCTTTTGATGTACTTTGTGAAAAAGTATGG 1982
Db 2074 GCGACACATCACCAAGCTGAAGCCCTGGAGCCCTTTTGATGTACTTTGTGAAAAAGTATGG 2133
Qy 1983 CTGGCCCCATGAAGATGCTGCACAGTTTACAGATTTCTCGATCCCGATGTTAGAAATGCT 2042
Db 2134 CTGGCCCCATGAAGATGCTGCACAGTTTACAGATTTCTCGATCCCGATGTTAGAAATGCT 2193
Qy 2043 TCCAGAAAAACGAGCTCAGCTGGCGAATGCTTCGGCATCTCTGTTGAAATCT 2097
Db 2194 TCCAGAAAAACGAGCTCAGCTGGCGAATGCTTCGGCATCTCTGTTGAAATCT 2245

RESULT 8

US-09-880-107-3294
; Sequence 3294, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3294
; LENGTH: 4326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U09564
US-09-880-107-3294

Query Match 30.1%; Score 631.4; DB 9; Length 4326;
Best Local Similarity 60.4%; Pred. No. 7.1e-156;
Matches 1170; Conservative 0; Mismatches 671; Indels 96; Gaps 4;
Qy 160 CCGAGAGCCAGAGGAGAGATCCTGGATCAGATGATGAGGAGCAGAGACCCCTGGGAC 219
Db 232 CCAGAGCAGGAGAGAGAGATTTCTGGGATCTGATGATGATGAGCAAGAGATCTTAATGAT 291
Qy 220 TACTTCAAGGTGGATATCATCCAGTGAATAATTTGAGACCTCTTCAATGCCCGGTATCAT 279
Db 292 TATTGTAAGGAGGTATCATCTTGTGAAATTTGAGATCTATTCAATGGAGATACCAT 351
Qy 280 GTTATTAGAAAGCTTTGGATGGGGCAGCTTCTCTACTGTCTGCTGTGCTGGATATGACAG 339
Db 352 GTGATCCGAAAGTTAGGCTGGGGACATTTTCAACAGATATGTTATCATGGGATATTCAG 411

QY 340 GGGAAAGATTGTTGCAATGAAGTGTGTAAGAGTGTCCAGCATTATACCGAGACGCC 399
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QY 400 TTGGATGAATTAATAATTGCTCAATGTTTGGAGAAAGTATCCAGTGCACCAACAAA 459
Db 472 CTAGATGAATCCGGTGTGCTGAAGTCAGTTCGCAATTCAGACCCCTTAATGATCCAAATAGA 531
QY 460 GACATGTTGGTCCAGCTCATTGACGACTTCAAGATTTTCAGGCAATGGAATGATATGTC 519
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QY 520 TGCATGTTCTCGAAGTACTTGGCCACCATTCTCTCAAGTGGATCATCAATCCAACTAT 579
Db 592 TGCATGTTCTCGAAGTACTTGGCCACCATTCTCTCAAGTGGATCATCAATCCAACTAT 651
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Db 712 TATTTACATACCAAGTGCAGTATCATTTCACTGATGATTAAGTGCAGGCTCTTCAAGGTTTATGAT 771
QY 700 TGTGTGATGATGATATGTGAGAGAAATGGCAGTGCAGGCTCTTCAAGGTTTATGAT 759
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QY 1240 GATGATGAAGAGACTGCCCCAATCTGAGGAAATAATAATTTGATGAGGCAATGAGAA 1299
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Db 1363 TCTGAGGTGTCACACACCATGGTGTGCCAGTCTTCTCAACTGTAGGTGATTCAGT 1422
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Db 1423 GAAC-----AACACATTAGCCAACTTCAAGAAAGCAATTCGGGC 1460
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Db 1516 AAAGGAAATCCACGGCTGGAAATTTTCTTGTAAATCCCTTTGAGCCCAAAATATGCGAA 1575
QY 1600 AAAATTAGATTAATAATTTGACTGCGGAAATCTTTTGGGTGCAATAACACTTCCAG 1659
Db 1576 AAGCTCAAGGTGAAGATTTGCTGACCTTTGGAATCTTGTGGGTGCAACAACTTTCACT 1635
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QY 1720 ACCCTGCGGACATCTGGAGCACGGCGTGAATGAGCTTTGAGCTGGCAACGGGAGATTA 1779
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Db 1756 TTGTTGAACCTCATTTAGGGGAAGAGTACTCGAGATGAAGATCACATTTGCTATGATC 1815
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Db 1816 ATAGAACTTTCTGGGGAAGGCTCTCGCAAGCTCATTTGGCGAGGAAATAATTTCAAGGAA 1875
QY 1900 TTCTCAATCCAGAGAGAGAACTGGGACATCATCAACAGCTGAAGCCCTGAGGCTCTTT 1959
Db 1876 TTTTTCACAAAAGAGTGAACCTGAAACATATACGAAGCTGAAACCTTTGGGGCTTTT 1935
QY 1960 GATGACTTTGGAAGAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2019
Db 1936 GAGGTTCTAGTGGAGAGTATGAGTGTCTCAGGAAGAGGAGCTGGCTTTCACAGATTC 1995
QY 2020 CTGATCCCGATTTAGAAATGTTTCCAGAAACGAGCCTCAGCTGGCGAAATGCTTCGG 2079
Db 1996 TTACTGCCATTTTGGAGCTGATCCCTGAGAGAGAGCCACTGCGCGAGTGTCTCCGG 2055
QY 2080 CATCCTTGGTGAATTC 2096
Db 2056 CACCTTGGCTTAATC 2072

RESULT 9

US-10-172-118-875
; Sequence 875, Application US/10172118
; Publication No. US20030224374A1

GENERAL INFORMATION:

; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yundong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene

TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

FILE REFERENCE: 9301-175-999

CURRENT APPLICATION NUMBER: US/10/172,118

CURRENT FILING DATE: 2002-06-14

PRIOR APPLICATION NUMBER: 60/380,770

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 2699

SEQ ID NO 875

LENGTH: 4326

TYPE: DNA

ORGANISM: Homo sapiens

PUBLICATION INFORMATION:


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; DATABASE ACCESSION NUMBER: NM 003137
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-875

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Query Match	30.1%;	Score 631.4;	DB 15;	Length 4326;
Best Local Similarity	60.4%;	Pred. No. 7.1e-156;		
Matches 1170; Conservative	0;	Mismatches 671;	Indels 96;	Gaps 4;

Qy	160	CCGAGCCAGAGGAGGAGATCCTGGGATCAGATCATGAGGAGCAAGAGGACCTTGCCGAC	219
Db	232	CCAGAGCAGGAAGAGGAGATCTCGGATCTGATGATGAGCAAGAGATCTCTTAATGAT	291
Qy	220	TACTGCAAAAGGTGGATATCATCCAGTCGAAAATGCGACCTCTTCAATGGCGGTATCAT	279
Db	292	TATTGTAAAGGAGGTATCATCTTGTGAAAATGAGATCTATTCAATGGGAGATACAT	351
Qy	280	GTTATTAGAAAGCTTGGATGGGGCACTTCTTACTGTCTGGCTGTCTGGGATATGCAG	339
Db	352	GTGATCCGAAAGTTAGGCTGGGACACTTTTCAACAGATATGTTTATCATGGGATATTTCAG	411
Qy	340	GGGAAAGATTTGTTGCAATGAAAGTTGTAAAGAGTCCAGCATTTATACGGAGACAGCC	399
Db	412	GGGAAAGAAATTTGTGGCAATGAAAGTAGTTAAAGTGTCTGAACATTTACACTGAAACAGCA	471
Qy	400	TTGATGAAATTAATAATTTGCTCAAAATGTGTTCCGAAAAGTGTATCCAGTGACCCAAACAAA	459
Db	472	CTAGATGAATCCGGTTTGCTCAAGTCAGTTCGCAATTCAGACCCTAATGATCCAAATAGA	531
Qy	460	GACATGTGTTCAGCTCATTTGACGACTTCAAGATTTTCAGGCATGAATGGGATACATGTC	519
Db	532	GAATGCTTGTTCAACTACTAGATGACTTTTAAAAATATCAGGAGTTAATGAAACACATATC	591
Qy	520	TGCATGCTCTCGAAGTACTTGGGCCACATCTCTCAAGTGGATCATCAATCCAACTAT	579
Db	592	TGCATGTTATTTGAAGTTTGGGGCATCATCTGCTCAAGTGGATCATCAATCCAAATAT	651
Qy	580	CAAGCCCTCCAGTACGTTGTGCAAGAGTATCATTCGACAGGTCTTCAAGGGTTAGAT	639
Db	652	CAGGGCTTCCACTGCCTTGTGTCAAAAAATTAATTCAGCAGTGTTCAGGGTCTTGAT	711
Qy	640	TACTTACACAGTAAAGTGAAGATCATTTCTATCTGACATAAAGCCGGAAAAATCTTGTGATG	699
Db	712	TATTTACATACCAAGTCCGCTATCATCCACACTGACATTAACCCAGAGAACATCTTATTG	771
Qy	700	TGTGTGATGATGCATATGTGAGAAAGTATGCGAGCTGAGCCCTGAGTGGCAGAAAGCA	759
Db	772	TCAGTGAATGAGCAGTACATTTGGAGGGTGGCTCGAAGCAACAGAAATGGCAGCGATCT	831
Qy	760	GGTGCTCTCTCTCCTCAGGCTCTGAGTACAGTACGGCTCCACAGCAGAAACCTTATAGGA	819
Db	832	GGAGCTCTCCGCCCTTCGGATCTGCGATCTGATCTGCTCCCCAGCCTTAACAGCTGAC	891
Qy	820	AAAATATCTTAAAAACAAAAAGAAAACTGAAAAAGAAAAACAGAAAGAGCGGTGAGTTA	879
Db	892	AAAATGTCAAGAAATAAGAAAGAGAAATTTGAAGAAAGAAAGCAGAGCGCCAGGCAGAATTA	951
Qy	880	TTGAGAGCGCCTGCAGGCGATAGAGATTTGGAGCAGAGCTGAAAGGAAATATAA	939
Db	952	CTAGAGAGCGAATGCAAGGAAATTTGAGAAATGAGAAAGAGTCCG-----	997
Qy	940	GAAGAAAAACATCACCTCAGCTGCACCTTCCAATGACCAGGATGGCGAATACTGCCCAGAG	999
Db	998	-----GCCTGGCCHAAAAAGACCAAC	1020
Qy	1000	GTGAAACTTAAAAACACAGGATTAAGAGAGCGGCTGAGGCGAGACTGCAAGGACAAT	1059
Db	1021	AAGCAAGAAAGAAATCAGAGAGTCTCTGTTGAAAGAGCCCTTGAAGAGAGAACCCACCTTAATAA	1080
Qy	1060	GGTGAAGCTGAGGACCGAGAGAAAGAGATCTCTGAAAGAGAAAAACATTTGAAAAAGAT	1119
Db	1081	ATGACCCAGAAAAAATTTGAAGAGTCAAGTACCAATTTGGCCAGGATCAACCGCTTATGAA	1140
Qy	1120	GAAGATGATGTAGATCAGGAACCTTGCAGAACATAGACCCCTCAGTGGATAGAAATCACCTTAA	1179

RESULT 10
US-10-342-887-875
; Sequence 875, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:

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; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 875
; LENGTH: 4326
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-342-887-875

Query Match      30.1%; Score 631.4; DB 16; Length 4326;
Best Local Similarity 60.4%; Pred. No. 7.1e-156;
Matches 1170; Conservative 0; Mismatches 671; Indels 96; Gaps 4;

QY 160 CCGAGCCAGAGAGAGATCTGGGATCAGATGATGAGGACCAAGAGACCTCGGAC 219
DB 232 CCAGACAGGAGAGAGATCTGGGATCTGATGATGATGAGGAGATCCTAATGAT 291
QY 220 TACTGCAAGGTGGATATCATTCAGTGAATAATGGAGCTCTCAATGGCCGGTATCAT 279
DB 292 TATTGTAAGAGGATTCATCTTGTGAATAATGGAGATCTATCAATGGGAGATACCAT 351
QY 280 GTTATTAGAAAGCTTCGATGGGGGACATCTCTACTGTCTGGTCTGGTGGATATGCG 339
DB 352 GTGATCGGAAGTATGAGCTGGGACACTTTCAACAGTATGTTATCATGGGATATTCAG 411
QY 340 GGGAAAGATTTCTGCAATGAAAGTTGAAAGTGGCCAGCATATATACGAGACGCC 399
DB 412 GCGAAGAAATTTGTGCAATGAAAGTAGTTAAAGTGTGAAATTTACATGAAACAGCA 471
QY 400 TTGGATGAATAAATTTGCTCAATGTTTCGAGAAAGTATCCAGTGCACCAACAAA 459
DB 472 CTAGATGAATTCGGTTGCTGAAAGTCAAGTTTCGCAATTCAGACCTTAATGATCCAAATAGA 531
QY 460 GACATGTTGTCAGGCTCATTTGACGACTTCAAGATTTTCAGGCAATGATGGGATACATGTC 519
DB 532 GAATGTTGTTCAACTACTAGATGACTTTTAAATATATCAGGAGTTAATGGAACACATATC 591
QY 520 TGCATGTTTCGAAGTATGTCGACCATCTCTCAAGTGGATCATCAATCCAACTAT 579
DB 592 TGCATGTTTGAAGTTTGGGACATCATCTCTCAAGTGGATCATCAATCCAACTAT 651
QY 580 CAGGCTCTCCAGTACGTTGTTGAAGATATCATTCAGAGTCTCTTCAAGGTTTAGAT 639
DB 652 CAGGGCTTCCATGCTGTTGTTCAAAAAATTTATTCAGCAAGTGTATACAGGCTTTGAT 711
QY 640 TACTTACACAGTAAAGTCAAGATCATTTATCATGACATAAAGCCGGAATAATATCTTGATG 699
DB 712 TATTTACATACCAAGTCCGATCATCCACACTGACATTAACAGAGAAACATCTTATTG 771
QY 700 TGTGTGATGATGATATGAGAGAAATGGCAGCTGAGGCCATGAGTGGCAGAAAGCA 759
DB 772 TCAGTGAATGAGAGTACATTCGGAGGCTGCTGCAGAGCAACAGAAATGGAGCGCATCT 831
QY 760 GGTGCTCTCTCTCTCAGGCTCTGAGTGAAGTACCGCTCCACAGCAGAAACCTATAGGA 819
DB 832 GGAGCTCTCTCTCTCTCGGATCTGAGTCAAGTACTGCTCCAGGCTTAAACAGAGTAC 891

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QY 820 AAAATATCTAAAAACAAAAAGAAAAAACTGAAAAAGAAAAACAGAGAGGCGCTGAGTTA 879
DB 892 AAAATCTCAAGAAATAAGAGAAAGAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 951
QY 880 TTGGAGAGGCGCTGAGAGATAGAGAAATTTGGAGCGAGAGAGCTGAAAGGAAAAATAA 939
DB 952 CTAGAGAGAGCGAATGAGAGAAATTTGAGAGAAATGAGAGAAAGAGTCGG----- 997
QY 940 GAAGAAAAACATCACTCAGCTGACCTTCCATATGACCAAGATGGCGGAATATCTGCCAGAG 999
DB 998 -----GCCCTGGGCAAAAAAGACCAAAAC 1020
QY 1000 GTGAAATAAAAAACAACAGGATTAGAGGAGGCGGCTGAGCGACAGACTCCAAAGGACAAT 1059
DB 1021 AAGCAAGAGAGATCAGAGAGTCTCTGTTGAAAGACCTTTGAAAGAGAAACCCACCTAATAA 1080
QY 1060 GGTGAGCTGAGCAGCAGGAGAGAGAGAGATGCTGAGAAAGAAAAACATTTGAAAAAGAT 1119
DB 1081 ATGACCCCAAGAAAAACTTTGAGAGTCAAGTACCATTTGGCCAGGATCAACGCTTATGGAA 1140
QY 1120 GAAGATGATGTAGATCAGGAACTTTGCAACATAGACCTTACGTGGATAGATCACTTAA 1179
DB 1141 CGTGATACAGAGGTGTGTCAGCAGAAATTAATTGCAATGGAGTGAATTGAAGTCATTAAT 1200
QY 1180 ACCAATGGCCATATTGAGATGGCCCATTTCTACTGGAGCAGCAACTTGGACGATGAAGAT 1239
DB 1201 TATACTCAGAACAGTAATAATGAACATTTGAGACATTAAGAGGATCTACATAATGCTAAT 1260
QY 1240 GATGATCAAGAGAGCTCCCAAACTCTGAGGAAATATAATCTTGTATGAGCCAAATGCAAGAA 1299
DB 1261 GACTGTGATGTCGAAATTTGAATCAGGAATCTAGTTTCTTAAGTCTCCCAATGGAGA- 1319
QY 1300 AGTGATTTACATATAGCAGCTCTTATGAAACAATTCATGTTGAATTTGCCAAATGGACGA 1359
DB 1320 -----CAGCAGCACATCTCAAGAAACAGACTCTTGTATACCTTATAACA 1362
QY 1360 CATAAATTTCCGAGTCACAGTCCAGAGTTTTTCCACCTCGTTGTTCTCTGTGATCCTTA 1419
DB 1363 TCTGAGGTGTCAGACACCATGTTGTCAGTCTTCTCACTGATGATGATGATGATGATGAT 1422
QY 1420 GAACTGTGGCTCGGCTCTGTCTTTCTGAGGGATCAACACTTACTGAGCAAGAGAG 1479
DB 1423 GAAC-----AACACATTTAGCCAACTTCAAGAAAGACTTCGGGC 1460
QY 1480 AGCAGTCCATCCCATGACAGAGCAGAGCGGTTTTCAGCTCCAGTCTGCGGATTTTGCCA 1539
DB 1461 AGAGATACCTGTGAAGATGAACAGAGCAAGAAACATAACGAGCACTGGACA-----AC 1515
QY 1540 AAAGCAAAACCCCGGACGCTGACTTGTGTTGATCCCTTGGATCCGCGGAATGCGAGAT 1599
DB 1516 AAAGGAAATTCACGGCTGGAAATTTTCTTGTAAATCCCTTTGAGCCAAAAAATGCGAAA 1575
QY 1600 AAAATTTAGAGTAAATAATTTGCTGAGCTGGGAAATGCTTGTGGTGCATAAACACTTCAG 1659
DB 1576 AAGCTCAAGGTGAAGATTTGCTGACCTTGGAAATGCTTGTGGTGCACAAACATTTTCACT 1635
QY 1660 GAAGACATCCAGACGCTGACTGACGCTCCATAGAGTTTAAATAGGAGCGGGGTACAGC 1719
DB 1636 GAAGATATTTCAAAACAAAGGCAATATCGTTCTTGGAAAGTCTTAATCGGATCTGGCTAAT 1695
QY 1720 ACCCTCTGGGACATCTGGAGCAGCGGCTGTATGGCAATTTGAGCTGGCAACGGGAGATTAT 1779
DB 1696 ACCCTCTGTGACATTTGGAGCAGCGCATGCTGGCTTTGAACTGGCCACAGGTGACTAT 1755
QY 1780 TTGTTTGAACCACTTTCTGGGGAAGACTATTTCCAGAGCAGGAGACCATAGCCACATC 1839
DB 1756 TTGTTTGAACCTCATTTCAAGGGAAGAGTACTCTGAGATGAAGATCACTATGCTGATGTC 1815
QY 1840 ATAGAGCTCTAGGAGTATTTCCAAAGGCACTTTGCTCTATCTGGAATAATATTTCTCGGAA 1899
DB 1816 ATAGAACTTTCTGGGAGAGTGTCTCGAAGCTCATTTGTGGCAGGAAAAATATTTCCAAGGAA 1875
QY 1900 TTCTTCAATTCGAGAGGAGAACTGCGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTT 1959

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Db	403	GTTCGAGAAAGTGATCCACGTGACCCCAACAAAGACATGGTGGTCCAGCTCATTTGACGAC	467
Qy	487	TTCAAGATTTTCAGGCATGAATGGGATACATGCTCTGCATGGTCTTCCGAAGTACTCTGGCCAC	546
Db	463	TTTAAGATTTTCAGGCATGAATGGGATACATGCTCTGCATGGTCTTCCGAAGTACTCTGGCCAC	522
Qy	547	CATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGCCCTCCCAAGTACGTTGTGTGAAG	606
Db	523	CATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGCCCTCCCAAGTACGTTGTGTGAAG	582
Qy	607	AGTATCATTTCCGACAGGTCCTTCAAGGGTTAGATTACTTACACAGTAAG-TGCAAGATCAT	665
Db	583	AGTATCATTTCCGACAGGTCCTTCAAGGGTTAGATTACTTACACAGTAAGTTGCAAGATCAT	642
Qy	666	TCATACTGACATAAAGCCGAAAAATATCTTGATGTGTGGATGATGATATGTGAGAAG	725
Db	643	ACNTACTGACATAAAGCCGAAAAATATCTTGATGTGTGGATGATGATATGTGAGAAG	702
Qy	726	AATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTCCTCTCTCTCAGGTCCTGTC	785
Db	703	AATGGCAGCTGANG--CCCTGATTGGCANAAGCAGGTCCTCC-NCTCCCTCAGGTCCTGTC	759
Qy	786	AGTCAGTACGGCTCCACAGCAGAACCTATAGGAAAAATCTAATAACAACAAAGAAAAA	845
Db	760	ANTGAATTACGGTCCCGCNGNAAAACTNTNGAAAAATTTCTAAAAACCNNGAAAAA	819
Qy	846	ACTGAAAAAGAAA	858
Db	820	AAANAAACNAAAA	832
RESULT 12			
US-10-252-157-374			
; Sequence 374, Application US/10252157			
; Publication No. US20030190640A1			
; GENERAL INFORMATION:			
; APPLICANT: Paris, Mary			
; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER			
; FILE REFERENCE: PA-0027-1 US			
; CURRENT APPLICATION NUMBER: US/10/252,157			
; CURRENT FILING DATE: 2002-10-01			
; PRIOR APPLICATION NUMBER: 60/295,048			
; PRIOR FILING DATE: 2001-05-31			
; NUMBER OF SEQ ID NOS: 501			
; SOFTWARE: PERL Program			
; SEQ ID NO 374			
; LENGTH: 4349			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: misc feature			
; OTHER INFORMATION: Incyte ID No. US20030190640A1 474724.5			
US-10-252-157-374			
Query Match 30.0%; Score 628.2; DB 15; Length 4349;			
Best Local Similarity 60.3%; Pred. No. 5e-155;			
Matches 1168; Conservative 0; Mismatches 673; Indels 96; Gaps 4			
Qy	160	CCGAGCCAGGAGGAGATCTCTGGGATCAGATGATGAGGAGCAGGACCTTCGCGAC	219
Db	232	CCAGCAGCAAGAGGAGATCTCTGGGATCTGATGATGATGAGCAAGATCTTAATGAT	291
Qy	220	TACTGCAAAAGTGGATATCATCCAGTCAAAAATGGAGACCTCTTCAATGGCGGTATCAT	279
Db	292	TATTGTAAAGGAGGTTATCATCTTTGTGAAAAATGGAGATCTTATTCAATGGGAGATACCAT	351
Qy	280	GTTATTAGAAGCTTGGATGGGGGCATCTCTACTGTCTGGCTGTCTGGATATGAG	339
Db	352	GTGATCCGAAGTTAGGCTGGGGACCTTTTCAACAGTATGGTTATCATGGGATATTCAG	411
Qy	340	GGGAAAAAGATTTGTTGCAATGAAAGTTGTAAAAAGTGCACAGCATTTATACGGAGACGCC	399

Db 412 GGGAAAGAAATTTGTGGCAATGAAAGTAGTTAAAGTGTGTAACATTAACCTGAAACAGCA 471
Qy 400 TTGGATGAAATAAATTTGCTCAATTTGCTTCCAGAAAGTGTATCCAGTGTACCCCAACAAA 459
Db 472 CTAGATGAAATCCGGTTGCTGAGTCAGTTCGCAATTCAGACCTTAATGATCCAAATAGA 531
Qy 460 GACATGGTGTCCAGCTCATTTGACCGAATTCAGAGATTCAGGCATGAATGGGATACATGTC 519
Db 532 GAAATGGTGTTCACCTACTAGATGACTTTAAATATCAGGAGTTAAATGGAAACATATC 591
Qy 520 TGCTAGTGTTCGAAGTACTTGGCCACCATCTCCCTCAAGTGGATCATCAATCCAACTAT 579
Db 592 TGCTAGTGTTCGAAGTACTTGGCCACCATCTCCCTCAAGTGGATCATCAATCCAACTAT 651
Qy 580 CAAGCCCTCCCAAGTACTTGGCCACCATCTCCCTCAAGTGGATCATCAATCCAACTAT 639
Db 652 CAGGGCTTCCCTGCTTGTGCTGAAAGATATCATTTCCAGAGTCTTCAAGGGTTAGAT 711
Qy 640 TACTTACACAGTGAAGTCAAGATCATTTCACTGACATATAAGCCCGGAAATATCTTTGATG 699
Db 712 TATTTACATACCAAGTGGCGTATCATCCACATGACATTTAAACAGAGAAACATCTTTATG 771
Qy 700 TGTGTGATGATGATATGTGAGAGAAATGGCAGCTGAGGCCACCTGAGTGGCAGAAAGCA 759
Db 772 TCAGTGAATGAGCAGTACATTCGGAGGCTGGCTGCAGAAAGCAAGAAATGGCAGCGATCT 831
Qy 760 GGTGCT 819
Db 832 GAGCT 891
Qy 820 AAAATATCTTAAAAAACAAGAAAGAACTGAAAAAGAAACAGAAAGAGCAGGCTCAGTTA 879
Db 892 AAAATGTCAAAGAAATGAAGAAAGAAATTTGAAGAAAGAAAGCAAGCGCCAGGCAGAAATTA 951
Qy 880 TTGAGAGAGCGCTCAGAGATAGAGAAATTTGAGCGGAGAGCTGAAAGGAAATTAATA 939
Db 952 CTAGAGAGCGAATGAGGAAATTTGAGGAAATTTGAGGAAATTTGAGGAAATTTGAGGAA 997
Qy 940 GAAGAAACATCACCTCAGCTGCACCTTCCATATGACAGGATGGCGAATCTACCTCCAGAG 999
Db 998 -----GCCCTGGGCAAAAAGACCAAC 1020
Qy 1000 GTGAAACTAAACAAACAGGATTTAGAGGAGCGGCTGAGGAGAGACTGCAAAAGCAAT 1059
Db 1021 AAGCAAGAAATCAGAGAGTCTGTTGAAAGACCTTTGAAAGAGAAACCCACCTTAATAA 1080
Qy 1060 GGTGAGCTGAGCAGCAGAGAGAGAGAGATGCTGAGAAAGAAACATTTGAAAGAT 1119
Db 1081 ATGACCCAGAAAGAACTTTGAGAGTCAAGTACCATTTGGCCAGGATCAAAACGCTTATGAA 1140
Qy 1120 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1179
Db 1141 CGTGATACAGAGGTTGTCAGAGAAATTAATTCATGAGTGAATGAGTCAATTAAT 1200
Qy 1180 ACCAATGGCCATATTTAGAAATGGCCCATTTCTCACTGGAGCAGCAACTGGACGATGAAGAT 1239
Db 1201 TATACTCAGAACAGTAATGAACATTTGAGACATTAAGAGGATCTACATAATGCTAAT 1260
Qy 1240 GATGATGAAGAGACTGCGCCAAATCTCTGAGGAATATAATCTTGATGAGGCAATGAGAA 1299
Db 1261 GACTGTGATGTCCAAATTTGAATCAGGAATCTAGTTTCTTAAGCTCCCAAAATGGAGA- 1319
Qy 1300 AGTGATTACATATAGCAGCTCTTATGAACAAATCAATGGTGAATTTGCCAATGAGCA 1359
Db 1320 -----CAGCAGCAGATCTCAAGAAACAGACTTTGTACACTATAACA 1362
Qy 1360 CATAAATTTCCGAGTCAAGTTCCAGAGTTTCCACCTCGTTGTTCTCTGGATCTTTA 1419
Db 1363 TCTGAGGTCTCAGACACCATGTTGTCAGTCTTCTCACTGATGAGTCAATCACT 1422
Qy 1420 GAACTGTGGCTGGGCTCTGTGCTTTCTGAGGATCACCCTTACTGAGCAGAGGAG 1479
Db 1423 GAAC-----AACACATTAGCCCACTTCAAGAAAGCATTTGGGCG 1460

Qy 1480 AGCAGTCCATCCCATGACAGAAAGCAGAAACGGTTTTCAGCCTCAGTACTGCGGATTTGCCA 1539
Db 1461 AGAGATACCTGTGTAAGATGAACAAGAGCAAGAAACATAACCGACCTTGGACA-----AC 1515
Qy 1540 AAAGCAAAACCCCGGAGCTGACTTTGTTGTTGTAATCCCTTGGATCCCGGAAATGCAGAT 1599
Db 1516 AAAGGAAATCCACGGCTGGAAATTTTCTGTTAATCCCTTGGATCCCGGAAATGCAGAA 1575
Qy 1600 AAAATTAGAGTAAAAATTTGCTGACCTGGGAAATGCTTGTGGTGCATATAACACTTTACG 1659
Db 1576 AAGCTCAGGTGAAGATTTGCTGACCTTGGAAATGCTTGTGGTGCACAAACATTTCACT 1635
Qy 1660 GAAGACATCCAGACCGCTCAGTACCGCTCCATAGAGGTTTTAAATAGGAGCGGGPACAGC 1719
Db 1636 GAAGATATTCACAAAGGCAATATCGTTCTTGGAAAGTTCTAATCGGATCTGGCTATAAT 1695
Qy 1720 ACCCTGGGACATCTGGAGCAGCGCTGATGATGCAATTTGAGCTGGCAACCGGAGATTAAT 1779
Db 1696 ACCCTGCTGACATTTGGAGCAGCGCATGCAATGCGCTTTGAACTGGCCACAGGTGACTAT 1755
Qy 1780 TTGTTGAACACATTTCTGGGAAAGACTATTTCCAGAGACGAAGACCAATAGCCCCACATC 1839
Db 1756 TTGTTGAACCTCATTCAGGGGAAAGATGACTCGAGATGAAGATCAATTTGCATTTGATC 1815
Qy 1840 ATAGAGCTGTAGGAGTATTTCCAGGCACTTTGCTCTATCTGGAATAATTTCTCGGAA 1899
Db 1816 ATAGAACTTTCTGGGAGGAGTCTCGCAAGCTCATTTGTCGAGGAAATAATTTCCAAGGAA 1875
Qy 1900 TTCTTCAATCCAGAGGAGAACTGGGACATCATCAGAGCTGAGAGCTTGGAGCTCTTT 1959
Db 1876 TTTTTCACAAAAAGGTGACCTGAAACATATACAGAGCTGAAACCTTTGGGCGCTTTT 1935
Qy 1960 GATGTACTTTGGAAAAAGTATGGCTGGCCCATGAAGATGCTGCACAGTTTACAGATTTT 2019
Db 1936 GAGTTCTAGTGGAGAGTATGAGTGTGTCGAGGAGAGGAGGAGCTTGGCTTTCACAGATTT 1995
Qy 2020 CTGATCCCGATTTAGAAATGTTTCCAGAAACAGAGCTCAGTGGGCAATGCTTCGG 2079
Db 1996 TTACTGCCCATGTTGGAGCTGATCCTCGAAGAGAGACCTGCGCGGAGTGTCTCGG 2055
Qy 2080 CATCTTGGTTGAATTC 2096
Db 2056 CACCTTGGCTTAATTC 2072

RESULT 13

US-09-814-353-21987
; Sequence 21987, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:

; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 21987

LENGTH: 4639

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

LOCATION: 4427-4428, 4429, 4430, 4431, 4432, 4433, 4434, 4435, 4436,

LOCATION: 4437, 4438, 4439, 4440, 4441, 4442, 4443, 4444, 4445, 4446,

LOCATION: 4447, 4448, 4449, 4450, 4451, 4452, 4453, 4454, 4455, 4456,

LOCATION: 4457

OTHER INFORMATION: n = A,T,C or G

US-09-814-353-21987

Query Match 30.0%; Score 628.2; DB 10; Length 4639;

Best Local Similarity 60.3%; Pred. No. 5.2e-155;

Matches 1168; Conservative 0; Mismatches 673; Indels 96; Gaps 4;

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QY 160 CCGGAGCCAGGAGGAGATCTGGGATCAGATGATGAGGAGCAAGAGGACCTGGGAC 219
DB 220 CCAGAGCAGAGAGAGAGATCTGGGATCTGATGATGATGAGCAGAGATCCTAATGAT 279
QY 220 TACTGCAAGAGGTGATATCATCCAGTGAAATTTGGAGACCTCTTCAATGGCCGGTATCAT 279
DB 280 TATTGTAAGGAGGTATCATCTGTGAAATTTGGAGATCTATTCAATGGGAGATACCAT 339
QY 280 GTTATTAGAAAGCTGGATGGGGGACCTTCTCTACTGTCTGGTGTGGGATATGCGAG 339
DB 340 GTGATCCGAAAGTTAGGCTGGGGGACATTTTCAACAGTATGTTATCATGGGATATTCAG 399
QY 340 GGGAAAGATTTGTCATGAAGTTGTAAGGTGCAAGGTCGCCAGCATATACGGAGCAGCC 399
DB 400 GGGAAAGATTTGTCATGAAGTTGTAAGGTGCAAGGTCGCCAGCATATACGGAGCAGCA 459
QY 400 TTGGATGAAATATAAATTTGCTCAATGTGTCGAGAAAGTGATCCAGTCAGCCCAACAA 459
DB 460 CTAGATGAATCCGGTGTGTCAGTCAGTTCGCAATTCAGACCTTAATGATCCAAATAGA 519
QY 460 GACATGGTGGTCAGCTCATGACGACTTCAAGATTTCAAGATTTCAAGGATGAATCGGATACATGTC 519
DB 520 GAAATGGTGTTCACACTACTAGATGATCTTAAATATACAGGAGTTAATGGAAACACATATC 579
QY 520 TGCATGGTCTTCAAGTACTTGGCCACCATCTCTCAAGTGCATCAATCCAATCACTAT 579
DB 580 TGCATGGTATTTGAAGTTTGGGGCATCATCTGCTCAAGTGCATCAATCCAATCACTAT 639
QY 580 CAAGGCTCCAGTACGTTGTGTAAGAGTATCATTCGACAGTCTCTTCAAGGTTAGAT 639
DB 640 CAGGGCTCCAGTACGTTGTGTAAGAGTATCATTCGACAGTCTCTTCAAGGTTAGAT 699
QY 640 TACTTACACAGTAAGTGCAGATCATTCATCTACTGATCAATAAGCCGGAATATCTTTGATG 699
DB 700 TATTTACATACCAAGTCCGATCATCCACACTGACATTAACACAGAGAACATCTTTATG 759
QY 700 TGTGTGGATGATGATATGTGAGAGAAATGGCAGCTGAGGCCCATCTGAGTGGCAGAAAGCA 759
DB 760 TCAGTGAATGAGCAGTACATTCGGAGGCTGGCTGCAGAAAGCAACAGAAATGGCAGCATCT 819
QY 760 GTGTCTCTCTCTTTCAGGCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 819
DB 820 GGAGCTCTCTCTCTTTCAGGCTCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 879
QY 820 AAAATACTAAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 879
DB 880 AAAATGCAAGAAATGAAGAGAAATTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939
QY 880 TTGAGAGAGCGCTGAGGAGATGAGAGAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 939
DB 940 CTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 985
QY 940 GAAGAAACATCACCTCAGCTGACCTTCCATGATCAGGATGGCGAATACTGCCAGAG 999
DB 986 -----GCCCTGGGCAAAAAGACCAAAAC 1008
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Qy 2080 CATCCTGGTTGAATTC 2096
Db 2044 CACCCCTGGCTTAATTC 2060

RESULT 14

US-10-029-386-9677
; Sequence 9677, Application US/10029386
; Publication No. US20030194704A1

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: GENERAL INFORMATION:
: APPLICANT: Penn, Sharron G.
: APPLICANT: Rank, David R.
: APPLICANT: Hanzel, K.
: TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
: TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
: FILE REFERENCE: AEMICA-X-2
: CURRENT APPLICATION NUMBER: US/10/029,386
: CURRENT FILING DATE: 2001-12-20
: NUMBER OF SEQ ID NOS: 34288
: SOFTWARE: Annonax Sequence Listing Engine vers. 1.1
: SEQ ID NO 9677
: LENGTH: 574
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: MAP TO CHR8.3
: OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9
: OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.7
: OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.6
: OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.9
: OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.7
: OTHER INFORMATION: SWISSPROT HIT: Q9UPE1, EVALUATE 1.00e-59
: OTHER INFORMATION: NT HIT: g114752654, EVALUATE 0.00e+00
: OTHER INFORMATION: EST_HUMAN HIT: AI038250.1, EVALUATE 0.00e+00
: US-10-029-386-9677

```

Query Match 23.3%; Score 488.6; DB 15; Length 574;
Best Local Similarity 92.9%; Pred. NO. 1.5e-118;
Matches 536; Conservative 0; Mismatches 34; Indels 7; Gaps 2;

311	Qy	CTACTGCTGGCTGTCTGGGATATGACGGGAAAGAATTTGTTGCCAATGAAGTTGTAA	370
1	Db	CTACTGCTGGCTGTCTGGGATATGTAGGGGAAAGAATTTGTGCAATGAAGTTGTAA	60
371	Qy	AAAGTGCCACGATTTATACGGAGACAGCCTTTGGATGAAATAAAATTTGCTCAATCTGTTTC	430
61	Db	AAAGTGCTCAGCGTGATACAGACACAGCCTTTGGATGAATAAATTTGCTCAATGTGTTTC	120
431	Qy	GAGAAAGTGATCCAGTGACCCAAACAAAGAATGGTGGTCCAGCTCATATGACGACTTCA	490
121	Db	GAGAAAGTTATCCAGTGACCCAAACAAAGAATGGTGGTATCCAGCTCGTT---GACTTCA	177
491	Qy	AGATTTTCAGGCATCAATGGGATCATGTCGCATGGTCTTCGAGTACTTGGCCACCACATC	550
178	Db	AGATTTTCAGGCATGAATGGGATCATGTCGCATGGTCTTGGAGTACTTGGCCACCACATC	237
551	Qy	TCCTCAAGTGGATCATCAAAATCCAAATCAAGGCCT---CCCAAGTACGTTGTGTGAAG	606
238	Db	TCCTCAACTGGATCATCAAGTTCAACTATCAAGGCCTCCCAAGTACGTTGTGTGAAG	297
607	Qy	AGTATCATTTGCACAGGTCTTCAGGGTTAGATTACTTTACACAGTAAGTGCAGAGTCAAT	666
298	Db	AGTATCATTTGACATTTCCCTTCAAGGGTTAGAAATCTACACAGTAAGCAAGAATTACT	357
667	Qy	CATACTGACATAAAGCCGGAAAAATCTTTGATGTGTGTGGATGATGCATATGTGAGAAGA	726
358	Db	CATACTGACATAAAGCCGAAAAATCTTTGATGTGTATGGATGATGCATATGTGAGAAGA	417
727	Qy	ATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCCTCCTCCTTCAGGGTCTGGA	786
418	Db	ACGGCAGCTGAGACCACTGAGGGGCGAAGAAGCAGGTATTCCTCCTCCTTCAGGGTCTGGA	477
787	Qy	GTGAGTACGGCTCCACAGCAGAAACCTATAGAAAAATATCTTAAAAACAAAAGAAAAAA	846

451 AAGTTGTAAGTCCAGCATTTATACGAGACAGCCTTGATGAAATAAATTTGCTC 510
421 AAATGTGTCGAGAAAGTATCCAGTACCCAAACAAAGACATGGTCCAGCTCAAT 480
511 AAATGTGTCGAGAAAGTATCCAGTACCCAAACAAAGACATGGTCCAGCTCAAT 570
481 GACGACTTCAAGATTTACAGCATGAATGGGATACATGCTGATGGTCTTCAAGTACTT 540
571 GACGACTTCAAGATTTACAGCATGAATGGGATACATGCTGATGGTCTTCAAGTACTT 630
541 GGCACCACTCTCCTCAAGTGGATCAATCAATCAATCAATCAAGGCTCCAGTACTGTTGT 600
631 GGCACCACTCTCCTCAAGTGGATCAATCAATCAATCAATCAAGGCTCCAGTACTGTTGT 690
601 GTGAAGAGTATCATTCGACAGTCTCTCAAGGTTAGATTACTTACACAGTAAGTGAAG 660
691 GTGAAGAGTATCATTCGACAGTCTCTCAAGGTTAGATTACTTACACAGTAAGTGAAG 750
661 ATCATTCTACTGACATAAAGCGGAAATATCTTGATGTGTGGATGATCATATGTG 720
751 ATCATTCTACTGACATAAAGCGGAAATATCTTGATGTGTGGATGATCATATGTG 810
721 AGAAGATCGCAGCTGAGGCCACTGAGTGGCAAGAGAGTGTCTCTCTCTTCAGGG 780
811 AGAAGATCGCAGCTGAGGCCACTGAGTGGCAAGAGAGTGTCTCTCTCTTCAGGG 870
781 TCTGAGTGTAGTACGCTCCACAGCAGAACCTATAGGAAATATCTTAAACAAAG 840
871 TCTGAGTGTAGTACGCTCCACAGCAGAACCTATAGGAAATATCTTAAACAAAG 930
841 AAAAACTGAAAGAAACAGAGAGCGAGGCTGAGTTATTGGAGAGCGCTTCAGGAG 900
931 AAAAACTGAAAGAAACAGAGAGCGAGGCTGAGTTATTGGAGAGCGCTTCAGGAG 990
901 ATAGAAGATTGAGCGAGAGCTGAAAGAAATTAATAGAGAGAAACATCACTCAGCT 960
991 ATAGAAGATTGAGCGAGAGCTGAAAGAAATTAATAGAGAGAAACATCACTCAGCT 1050
961 GCACCTTCAATGACAGAGTGGCAATATCTGCCAGAGGTGAATCTTAAACAAAG 1020
1051 GCACCTTCAATGACAGAGTGGCAATATCTGCCAGAGGTGAATCTTAAACAAAG 1100
1021 TTAGAGAGCGGCTGAGGCAGAGACTGCAAGGACAATGGTGAAGCTGAGGACCAAGAA 1080
1111 TTAGAGAGCGGCTGAGGCAGAGACTGCAAGGACAATGGTGAAGCTGAGGACCAAGAA 1170
1081 GAGAAAGAGATGCTGAGAAAGAAACATTTGAAAGAGATGAAGATGATAGATCAGAA 1140
1171 GAGAAAGAGATGCTGAGAAAGAAACATTTGAAAGAGATGAAGATGATAGATCAGAA 1230
1141 CTTGCGAACATGACCTCTGCTGATGATGATCACTTAAACCAATGGCCATTTGAGAT 1200
1231 CTTGCGAACATGACCTCTGCTGATGATGATCACTTAAACCAATGGCCATTTGAGAT 1290
1201 GGCCCACTTCTACTGGAGCAGCACTGGAGATGAAGATGATGATGAAGAGCTGCCCA 1260
1291 GGCCCACTTCTACTGGAGCAGCACTGGAGATGAAGATGATGATGAAGAGCTGCCCA 1350
1261 AATCCTGAGGAATATATCTTGATGAGCCAAATGCGAAGATGATTAACATATAGCAG 1320
1351 AATCCTGAGGAATATATCTTGATGAGCCAAATGCGAAGATGATTAACATATAGCAG 1410
1321 TCCTATGAAACAATTCATGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1380
1411 TCCTATGAAACAATTCATGTTGATGATGATGATGATGATGATGATGATGATGATGAT 1470
1381 TTCCAGAGATTTCCAGCTCGTTGCTCTGATGATGATGATGATGATGATGATGATGAT 1440
1471 TTCCAGAGATTTCCAGCTCGTTGCTCTGATGATGATGATGATGATGATGATGATGAT 1530
1441 GTGCTTCTGAGGATCACCACCTTACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
1531 GTGCTTCTGAGGATCACCACCTTACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1590

QY 1501 AGCAGAACGGTTTTCAGCTCCAGTACTGGGATTTGCAAAAGCAAAACCCGGCAGCT 1560
Db 1591 AGCAGAACGGTTTTCAGCTCCAGTACTGGGATTTGCAAAAGCAAAACCCGGCAGCT 1650
QY 1561 GACTTGTGTGTAATCCCTGGATCCCGGAAATGAGATTAATAATAGAGTAAATTTGCT 1620
Db 1651 GACTTGTGTGTAATCCCTGGATCCCGGAAATGAGATTAATAATAGAGTAAATTTGCT 1710
QY 1621 GACCTGGAAATGCTTGTGGTGCATAAACACATTCACGGAAGACATTCAGACCGCTCAG 1680
Db 1711 GACCTGGAAATGCTTGTGGTGCATAAACACATTCACGGAAGACATTCAGACCGCTCAG 1770
QY 1681 TACCGCTCCATAGAGGTTTAAATAGGAGCGGGTACAGCACCCCTGCGGACATCTGGAGC 1740
Db 1771 TACCGCTCCATAGAGGTTTAAATAGGAGCGGGTACAGCACCCCTGCGGACATCTGGAGC 1830
QY 1741 ACGCGGTGTATGGATTTAGCTGGCAACCGGAGATTAATTTGTTGAACCAATCTCTGGG 1800
Db 1831 ACGCGGTGTATGGATTTAGCTGGCAACCGGAGATTAATTTGTTGAACCAATCTCTGGG 1890
QY 1801 GAAGACTATTCCAGAGACGAAACACATAGCCCCACATCATAGAGCTGCTAGGCAATTT 1860
Db 1891 GAAGACTATTCCAGAGACGAAACACATAGCCCCACATCATAGAGCTGCTAGGCAATTT 1950
QY 1861 CCAAGGCACTTTGCTCTATCTGGAATAATTTCTCGGAATTTCTTCAATTCGAGAGGAA 1920
Db 1951 CCAAGGCACTTTGCTCTATCTGGAATAATTTCTCGGAATTTCTTCAATTCGAGAGGAA 2010
QY 1921 CTGGACACATCAGAGCTGAGCCCTGGAGCCCTTTGATGTACTTGTGGAAGATTTAT 1980
Db 2011 CTGGACACATCAGAGCTGAGCCCTGGAGCCCTTTGATGTACTTGTGGAAGATTTAT 2070
QY 1981 GCCTGGCCCCATGAAGATGCTGACAGTTTACAGATTTCTGTATCCCGATTTAGAAATG 2040
Db 2071 GCCTGGCCCCATGAAGATGCTGACAGTTTACAGATTTCTGTATCCCGATTTAGAAATG 2130
QY 2041 GTTCAGAAAAACGAGCCTCAGCTGGGAAATGCGCTTGGGATTCCTTGGTGAATTTCT 2097
Db 2131 GTTCAGAAAAACGAGCCTCAGCTGGGAAATGCGCTTGGGATTCCTTGGTGAATTTCT 2187

RESULT 2

US-10-207-973-1
; Sequence 1, Application US/10207973
; Patent No. 6753175
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/10/207,973
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3253
; TYPE: DNA
; ORGANISM: Human
US-10-207-973-1

Query Match 100.0%; Score 2097; DB 4; Length 3253;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGCTCCCGAAAGTCTGGCCATTTCAGGCCGAAAGCGAGGCCGAAAGAGAGAGAAA 60
Db 91 ATGAGCTCCCGAAAGTCTGGCCATTTCAGGCCGAAAGCGAGGCCGAAAGAGAGAGAAA 150
QY 61 CATCCGAAAAAGCCGAGGCTCAACAGAAAGCTCTTTAGTTCTCTCTCTCTCCACGCCCA 120
Db 151 CATCCGAAAAAGCCGAGGCTCAACAGAAAGCTCTTTAGTTCTCTCTCTCTCCACGCCCA 210

;; TITLE OF INVENTION: PROTEIN KINASE MOLECULES
;; NUMBER OF SEQUENCES: 12
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.
;; STREET: 3174 Porter Drive
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94304
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/016,000
;; FILING DATE: HERewith
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Billings, Lucy J
;; REGISTRATION NUMBER: 36,749
;; REFERENCE/DOCKET NUMBER: PF-0465 US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-855-0555
;; TELEFAX: 650-845-4166
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2791 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: HEARNOT01
;; CLONE: 307624
;; US-09-016-000-8

Query Match 96.5%; Score 2023.8; DB 2; Length 2791;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2028; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 63 TCCGAAAAAGCGGAGCTTCAACAGAAAGCTCTCTTAGTTCTCTCTCCCTCCACCGCCACC 122
DB 202 TTCAGAAAGCGCGAGCCTCAACAGAAAGCTCTCTTAGTTCTCTCTCCCTCCACCGCCACC 261
QY 123 ACCACACACCGCCACCTTTGCCAGACCCCAACCCCGGAGCCAGAGGAGATCCT 182
DB 262 ACCACACACCGCCCTTTGCCAGACCCCAACCCCGGAGCCAGAGGAGATCCT 321
QY 183 GGGATCAGATGATGAGGACAGAGGACCTCGGACTACTCCTCAAGGTGGATATCATCC 242
DB 322 GGGATCAGATGATGAGGACAGAGGACCTCGGACTACTCCTCAAGGTGGATATCATCC 381
QY 243 AGTGAATAATGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTTGGATGGG 302
DB 382 AGTGAATAATGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTTGGATGGG 441
QY 303 GCATTTCTACTGTCTGTGCTGTGGATATGACGGGGAAGAAAGTTGTTGCAATGAA 362
DB 442 GCATTTCTACTGTCTGTGCTGTGGATATGACGGGGAAGAAAGTTGTTGCAATGAA 501
QY 363 AGTTGTAATAAGTGGCCAGCATATACGGAGACAGCTTTGGATGAAATAAAATTTGCTCAA 422
DB 502 AGTTGTAATAAGTGGCCAGCATATACGGAGACAGCTTTGGATGAAATAAAATTTGCTCAA 561
QY 423 ATGTGTTCCAGAAAGTGATCCAGTGACCCCAACAAAGACATGTTGGTCCAGCTCATGA 482
DB 562 ATGTGTTCCAGAAAGTGATCCAGTGACCCCAACAAAGACATGTTGGTCCAGCTCATGA 621
QY 483 CGACTTCAAGATTTCAAGCATGATGGGATACATGCTGCTGCTTCCGAAGTACTTGG 542

DB 622 CGACTTCAAGATTTCAAGCATGATGGGATACATGCTGCTGATGCTTTCGAGTACTTGG 681
QY 543 CCACCATCTCTCTCAAGTGGATCATCAATCAACTATCAAGGCCCTCCAGTACGTTGTT 602
DB 682 CCACCATCTCTCTCAAGTGGATCATCAATCAACTATCAAGGCCCTCCAGTACGTTGTT 741
QY 603 GAAGAGTATCATTCGACAGGTCCTTCAAGGGTTAGATTACTTACACAGTAGTCAAGAT 662
DB 742 GAAGAGTATCATTCGACAGGTCCTTCAAGGGTTAGATTACTTACACAGTAGTCAAGAT 801
QY 663 CATTCTACTGACATTAAGCCGGAATAATCTTCTGATGTGTGTGATGATGATGATGATGAT 722
DB 802 CATTCTACTGACATTAAGCCGGAATAATCTTCTGATGTGTGTGATGATGATGATGATGAT 861
QY 723 AAGAATGGCAGCTGAGGCCACTGAGTGGCGAAGAGCAGGTGCTCTCTCTCTCTCAGGTC 782
DB 862 AAGAATGGCAGCTGAGGCCACTGAGTGGCGAAGAGCAGGTGCTCTCTCTCTCTCAGGTC 921
QY 783 TGCAGTGATGAGCTCCACAGCAGAAACCTTATAGGAAATAATCTTAAACCAAAAGAA 842
DB 922 TGCAGTGATGAGCTCCACAGCAGAAACCTTATAGGAAATAATCTTAAACCAAAAGAA 981
QY 843 AAACTGAAAAGAAACAGAGAGCGAGGCTGAGTATTGGAGAGCGCCTGCAGGAGAT 902
DB 982 AAACTGAAAAGAAACAGAGAGCGAGGCTGAGTATTGGAGAGCGCCTGCAGGAGAT 1041
QY 903 AGAAGAAATTTGAGCGGAGAGCTGAAAGGAAATAATAGAGAAACATCATCTCAGCTGC 962
DB 1042 AGAAGAAATTTGAGCGGAGAGCTGAAAGGAAATAATAGAGAAACATCATCTCAGCTGC 1101
QY 963 ACCTTCCAAATGACAGGATGGCGAATATCTGCCAGAGGTGAACTTAAACCAACAGGATT 1022
DB 1102 ACCTTCCAAATGACAGGATGGCGAATATCTGCCAGAGGTGAACTTAAACCAACAGGATT 1161
QY 1023 AGAGAGCGGCTGAGCGAGAGACTGCAGAGCAATGCTGAGCAATGCTGAGGACCCAGGAAGA 1082
DB 1162 AGAGAGCGGCTGAGCGAGAGACTGCAGAGCAATGCTGAGCAATGCTGAGGACCCAGGAAGA 1221
QY 1083 GAAAGAGATGCTGAGAAAGAAACATTTGAAAAAGATGAAGATGATGATGATGATGATGAT 1142
DB 1222 GAAAGAGATGCTGAGAAAGAAACATTTGAAAAAGATGAAGATGATGATGATGATGATGAT 1281
QY 1143 TCGGAAATAGACCCCTAGCTGATAGATCACTTAAACCAATGCGCATATTTGAAATGG 1202
DB 1282 TCGGAAATAGACCCCTAGCTGATAGATCACTTAAACCAATGCGCATATTTGAAATGG 1341
QY 1203 CCCATTCTCACTGGAGCAGCAACTGGACGATGAAGATGATGATGAAGAGACTGCCCAA 1262
DB 1342 CCCATTCTCACTGGAGCAGCAACTGGACGATGAAGATGATGATGAAGAGACTGCCCAA 1401
QY 1263 TCCTGAGGAATATATCTTGTATGAGCCAAATTCAGAAAAGTGAATTAACATATAGCAGTCT 1322
DB 1402 TCCTGAGGAATATATCTTGTATGAGCCAAATTCAGAAAAGTGAATTAACATATAGCAGTCT 1461
QY 1323 CTATGAACAAATTAATGTTGATTTGCCAAATGGAGCATAAAATTCGCGAGTCAAGTT 1382
DB 1462 CTATGAACAAATTAATGTTGATTTGCCAAATGGAGCATAAAATTCGCGAGTCAAGTT 1521
QY 1383 CCCAGATTTTCCACCTCGTTGTTCTCTGGATCTCTAGAACCTGTGGCTTGGCTCTGT 1442
DB 1522 CCCAGATTTTCCACCTCGTTGTTCTCTGGATCTCTAGAACCTGTGGCTTGGCTCTGT 1581
QY 1443 GCTTTCTGAGGATCAACCTTACTGTAGCAAGAGAGAGCAGTCCATCCCATGACAGAAG 1502
DB 1582 GCTTTCTGAGGATCAACCTTACTGTAGCAAGAGAGAGCAGTCCATCCCATGACAGAAG 1641
QY 1503 CAGAACGTTTTCAGCTCCAGTCTGCGGATTTGCCAAAGCAAAACCCGGGCGAGTGA 1562
DB 1642 CAGAACGTTTTCAGCTCCAGTCTGCGGATTTGCCAAAGCAAAACCCGGGCGAGTGA 1701
QY 1563 CTGTGTTGGTGAATCCCTCTGGATCCCGGAATGCGATAAATTTAGAGTAAATTTGCTGA 1622

Db 1702 CTTGTTGGTGAATCCCTCGATCCGCGGAATGCAGATAAAATTAGAGTAAATAATTCCTGA 1761
QY 1623 CTTGGGAAATGCTTGTGGTGCATAAACACTTCACGGAAGACATCCAGACGGTCACTA 1682
Db 1762 CTTGGGAAATGCTTGTGGTGCATAAACACTTCACGGAAGACATCCAGACGGTCACTA 1821
QY 1683 CGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTCGCGACATCTGGAGCAC 1742
Db 1822 CGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTCGCGACATCTGGAGCAC 1881
QY 1743 GCGGTGTATGGCATTTGAGCTGSCAACGGGAGATTATTTGTTGAACCCACATTTCTGGGA 1802
Db 1882 GCGGTGTATGGCATTTGAGCTGSCAACGGGAGATTATTTGTTGAACCCACATTTCTGGGA 1941
QY 1803 AGACTATTCAGAGACGAAGACACATAGCCACATCATAGAGCTGCTAGGACGATATCC 1862
Db 1942 AGACTATTCAGAGACGAAGACACATAGCCACATCATAGAGCTGCTAGGACGATATCC 2001
QY 1863 AAGGCATTTGCTCTATCTGGAATAATTTCTGGGAATTTCTTCAATCGCAGAGGAACT 1922
Db 2002 AAGGCATTTGCTCTATCTGGAATAATTTCTGGGAATTTCTTCAATCGCAGAGGAACT 2061
QY 1923 GCGACATCACCACAGCTGAAGCCCTGGAGCCCTTTTGATGTAATTTGTTGAAAAAGTATGG 1982
Db 2062 GCGACATCACCACAGCTGAAGCCCTGGAGCCCTTTTGATGTAATTTGTTGAAAAAGTATGG 2121
QY 1983 CTGGCCCATGAGATGCTGCACAGTTTACAGATTTCCCTGATCCCGATGTTAGAAATGTT 2042
Db 2122 CTGGCCCATGAGATGCTGCACAGTTTACAGATTTCCCTGATCCCGATGTTAGAAATGTT 2181
QY 2043 TCAGAAAAACGAGCTCAGCTGGCGAATGCGCTTCGGCATCCTTGGTTGAATTC 2097
Db 2182 TCAGAAAAACGAGCTCAGCTGGCGAATGCGCTTCGGCATCCTTGGTTGAATTC 2236

RESULT 4

US-08-264-002-1
; Sequence 1, Application US/08264002
; Patent No. 5559019
; GENERAL INFORMATION:
; APPLICANT: GUI, JIAN-FANG
; APPLICANT: FU, XIANG-DONG
; TITLE OF INVENTION: NOVEL PROTEIN SERINE KINASE, SRPK1
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLY HORN JUBAS & LUBITZ
; STREET: 1880 Century Park East, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 22-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN PH.D., LISA A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD3590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: SRPK1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 109..2073
; US-08-264-002-1

Query Match 30.1%; Score 631.4; DB 1; Length 4299;
Best Local Similarity 60.4%; Pred. No. 2.4e-160;
Matches 1170; Conservative 0; Mismatches 671; Indels 96; Gaps 4;

QY 160 CCGGACCCAGAGAGAGATCCTGGGATCAGATGATGAGGAGCAGGAGGACCCCTCGGAC 219
Db 232 CCAGAGCAGGAAGAGAGATCCTGGGATCTGATGATGAGGAGGATCCTTAATGAT 291
QY 220 TACTGCAAAAGTGGATATCATCCAGTGAAATTTGGAGACCTCTTCAATGCCGGTATCAT 279
Db 292 TATTGTAAAGGAGTTATCATCTTGTGAAATTTGGAGATCTATTCAATGGAGATACCAT 351
QY 280 GTTATTAGAAAGCTTGGATGGGGGACATCTCTACTGTCTGTGCTGTGCTGGGATATGCG 339
Db 352 GTGATCCGAAAGTTAGGCTGGGACACATTTTCAACAGATATGTTTATCATGGGATATTCAG 411
QY 340 GGGAAAAAGATTGTTGCAATGAAAGTTGTAAGAGTGGCCAGCATTTATACGGAGACAGCC 399
Db 412 GGGAGAAATTTTGGCAATGAAAGTAGTTAAAGTGTGAAATTTACATTTACACTGAAACAGCA 471
QY 400 TTGGATGAAATAAATTTGCTCAAAATGTTTCGAGAAAGTGTATCCAGTGCACCAACAA 459
Db 472 CTAGATGAATCCGGTTGCTGAAGTCAGTTTCGCAATTCAGACCTTAATGATCCAAATAGA 531
QY 460 GACATGGTGGTCCAGCTCATTCAGCAGCTTCAAGATTTTCAAGGATGAATGGGATACATGTC 519
Db 532 GAAATGGTTGTTCAACTACTAGATGACTTTAAATATATCAGGAGTTAATGGAAACACATATC 591
QY 520 TGCATGGTCTTCGAAAGTACTTGGCCACCATCTCTCAAGTGGATCATCAATCCAACTAT 579
Db 592 TGCATGGTATTTGAAAGTTTGGGGCATCATCTGCTCAAGTGGATCATCAATCCAACTAT 651
QY 580 CAAGGCCTCCAGTACGTTGTGTAAGAGTATCATTCGACAGGTCCTTCAAGGGTTAGAT 639
Db 652 CAGGGGCTCCACTGCTTGTGTCAAAAAATTTTACGCAAGTGTTCAGGGTCTTGAT 711
QY 640 TACTTACACAGTAAGTGAAGATCATTTCACTGACATATAAGCCGGAATAATTCCTGATG 699
Db 712 TATTTACATACCAAGTGGCGTATCATCCACATGACATTTAAACCCAGAGAACTCTTTATG 771
QY 700 TGTGTGGATGATCATATGTGAGAGAAATGGCAGCTGAGGCCCATCTAGTGGCAGAAAGCA 759
Db 772 TCAGTGAATGAGCAGTACATTCGGAGGCTGGCTGCAGAAAGCAACAGAAATGGCAGCATCT 831
QY 760 GGTGCTCTCTCTCTTCCAGGCTGTCAGTGAAGTACGGCTCCACAGCAGAAACCTATAGGA 819
Db 832 GGAGCTCTCTCCGCTTCCGATCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 891
QY 820 AAAATATCTAAAAACAAAAAGAAAACTGAAAAAGAAAACAGAAAGAGGAGGCTGAGTTA 879
Db 892 AAAATGTCAAAGAATAAGAAAGAAATTTGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 951
QY 880 TTGGAGAGCGGCTGCGAGAGATAGAGAAATTTGGAGCGGAGAGCTGAAGAGAAATAATA 939
Db 952 CTAGAGAGCGAAATGCGAGAAATTTGAGAAATTTGAGAAAGAGTCTGCG----- 997
QY 940 GAAGAAAAACATCACCTCAGCTGCACCTTCCAATGACAGGATGGCGAAATCTGCCAGAG 999
Db 998 -----GCCCTGGGCAAAAAGACCAAC 1020
QY 1000 GTGAAACTAAAAACCAACAGGATTTAGAGGAGGCGGCTGAGGAGAGAGCTCCAAAGGCAAT 1059
Db 1021 AAGCAAGAAGAAATCAGAGAGTCTCTGTTGAAAGACCCCTTGAAGAGAGAGACCCACCTAATAA 1080
QY 1060 GGTGAAGCTGAGGACCAAGAGAGAAAGAGATGCTGAGAGAGAAACATTGGAAGAAGAT 1119

Db 63657 TTGTTCTCTGGATCCTTAGAACCTGTGGCTGCGGCTCTGTGCTTTCTGAGGGATCACCA 63716
QY 1462 CTTACTGACGAGAGAGCAGTCCATCCCATGACAGAAAGCAGAACGGTTTTCAGCCTCC 1521
Db 63717 CTTACTGACGAGAGAGCAGTCCATCCCATGACAGAAAGCAGAACGGTTTTCAGCCTCC 63776
QY 1522 AGTACTGGGGATTGCCAAAAGCAAA 1547
Db 63777 AGTACTGGGGATTGCCAAAAGGTAA 63802

RESULT 8

US-09-173-581-10
; Sequence 10, Application US/09173581A
; Patent No. 6013455
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/173,581A
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 119819
US-09-173-581-10

Query Match 13.9%; Score 291.4; DB 3; Length 1427;

Best Local Similarity 70.2%; Pred. No. 1.1e-68;
Matches 391; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 1534 TTGCGAAAGCAAAACCCGGCAGCTGACTTTGTTGGTGAATCCCTCGATCCGGGAAT 1593
Db 800 TCGCCTAGCACACCATTCGGTGCCTCGAACCTCTGTTGTAACCCCTGGAGCCCCAAAT 859
QY 1594 GCAGATAAAATTAGAGTAAAAATTGCTGACCTGGGAAATGCTTTGTTGGTGCATAAACAC 1653
Db 860 GCAGATAAGATCAAGATCAAGATCGAGACCTGGGCAACGCCCTGCTGGGTGCACAAGCAC 919
QY 1654 TTCAGGAAGACATCCAGACGGTGCAGTACCGCTCCATAGAGTTTAAATAGGAGCGGG 1713
Db 920 TTCAGGAAGACATCCAGACTCGGAGTACCGGGCGCTGAGTGTGATCGGCCCGGAA 979
QY 1714 TACAGCACCCTCGGACATCTGGAGCAGCGGCTGTATGGCATTTTGGATGGCAACGGGA 1773
Db 980 TACGCCCCCGGACATCTGGAGCAGCAGCTGATGGCTTCGAGCTGGCCACTGGT 1039
QY 1774 GATTATTTGTTGAACCATTTCTGGGGAAGACTATTCCAGAGACGAAGACCATAGCC 1833
Db 1040 GACTACCTGTTGAGCGCATTTCTGGAGAAGACTACAGTCGTGATGAGGACCATCGCT 1099
QY 1834 CACATCATAGAGTGTAGCGAGTATCCAGGCACTTTGCTCTATCTGGAATAATTTCT 1893
Db 1100 CACATAGTGGAGCTTCTGGGGACATCCCCCAGCGCTTCGCCCTCTCAGGCCGCTATTCC 1159
QY 1894 CGGGAAATTTCTCAATCGCAGAGAGAACTCGGACACATCACCAGCTGAAGCCCTGGAGC 1953
Db 1160 CGGGAGTTCTTCAACCGGAGAGAGAGCTCGGCAATCCCAATCTCAAGCACTGGGCG 1219
QY 1954 CTCCTTGATGTTCTGTTGAAAGATATGGCTGGCCCATGAAGATGCTGCACAGTTTACA 2013

Db 1220 CTGTACGAGGTACTCATGTGAAAAGTACGAGTGGGCCCTTAGAGCGGCACACAGTTTCAGC 1279
QY 2014 GATTTCCTGTATCCCGATGTTAGAAATGTTCCAGAAAAACGAGCCTCAGCTGGCGAATGC 2073
Db 1280 GCCTTTCTGCTGCCATGATGATGATACATCCCCGAAAAGCGGCCAGTCCCGTGACTGC 1339
QY 2074 CTTCCGGCATCTTGGTT 2090
Db 1340 CTCCAGCACCCCTGGCT 1356

RESULT 9

US-09-420-915-10
; Sequence 10, Application US/09420915
; Patent No. 6264947
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/420,915
; EARLIER FILING DATE: 1998-10-20
; EARLIER APPLICATION NUMBER: US 09/173,581
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 119819
US-09-420-915-10

Query Match 13.9%; Score 291.4; DB 3; Length 1427;

Best Local Similarity 70.2%; Pred. No. 1.1e-68;
Matches 391; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 1534 TTGCGAAAGCAAAACCCGGCAGCTGACTTTGTTGGTGAATCCCTCGATCCGGGAAT 1593
Db 800 TCGCCTAGCACACCATTCGGTGCCTCGAACCTCTGTTGTAACCCCTGGAGCCCCAAAT 859
QY 1594 GCAGATAAAATTAGAGTAAAAATTGCTGACCTGGGAAATGCTTTGTTGGTGCATAAACAC 1653
Db 860 GCAGATAAGATCAAGATCAAGATCGAGACCTGGGCAACGCCCTGCTGGGTGCACAAGCAC 919
QY 1654 TTCAGGAAGACATCCAGACGGTGCAGTACCGCTCCATAGAGTTTAAATAGGAGCGGG 1713
Db 920 TTCAGGAAGACATCCAGACTCGGAGTACCGGGCGCTGAGTGTGATCGGCCCGGAA 979
QY 1714 TACAGCACCCTCGGACATCTGGAGCAGCGGCTGTATGGCATTTTGGATGGCAACGGGA 1773
Db 980 TACGCCCCCGGACATCTGGAGCAGCAGCTGATGGCTTCGAGCTGGCCACTGGT 1039
QY 1774 GATTATTTGTTGAACCATTTCTGGGGAAGACTATTCCAGAGACGAAGACCATAGCC 1833
Db 1040 GACTACCTGTTGAGCGCATTTCTGGAGAAGACTACAGTCGTGATGAGGACCATCGCT 1099
QY 1834 CACATCATAGAGTGTAGCGAGTATCCAGGCACTTTGCTCTATCTGGAATAATTTCT 1893
Db 1100 CACATAGTGGAGCTTCTGGGGACATCCCCCAGCGCTTCGCCCTCTCAGGCCGCTATTCC 1159
QY 1894 CGGGAAATTTCTCAATCGCAGAGAGAACTCGGACACATCACCAGCTGAAGCCCTGGAGC 1953
Db 1160 CGGGAGTTCTTCAACCGGAGAGAGAGCTCGGCAATCCCAATCTCAAGCACTGGGCG 1219
QY 1954 CTCCTTGATGTTCTGTTGAAAGATATGGCTGGCCCATGAAGATGCTGCACAGTTTACA 1219

Qy	1954	CTCTTTGATGTA	CTTTGGAAAAGT	TGGCTGGCCCCCAT	GAAAGTCTGCACAGTTTACA	2013
Db	1220	CTGTACGAGGTA	CTCATGGAAAAGT	ACGAGTGGCCCCCT	TAGACGAGGCCACACAGTTTCAGC	1279
Qy	2014	GATTTCTGATCCG	GATGTTAGAAAT	TGGTTCCAGAAAAA	CAGGCCTCAGCTGCGGGAATGC	2073
Db	1280	GCCTTTTCTGCTG	CCCATGAATGAGT	ATACATCCCGAAAA	AGCGGCCAGTGCCCGTGACTGC	1339
Qy	2074	CTTCGGCATCCTT	TGGTT			2090
Db	1340	CTCCAGACCCCT	TGGCT			1356

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RESULT 10
US-09-016-434-79
; Sequence 79, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
;

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	Query Match Best Local Similarity Matches	12.1%; 67.4%; 360;	Score 254; Pred. No. 1.1e-58; Conservative 0;	DB 4; Length 793; Mismatches 172; Indels 2; Gaps 2;
Qy	179	TCCTGGGATCAGATGATGAGAGCAAGAGACCTCTCGGACTACTGCAAAAGGTGGATATC	238	
Db	156	TTCTGGGCTCCGACGACGAGAACAGAGACCCCAAGACTACTGCAAGGGCGGCTACC	215	
Qy	239	ATCCAGTGAATAATTGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGAT	298	
Db	216	ACCCTGTGAAGATCGCGACGCTGTTCAATGGGCGGTACACGTTGGTGCNCNCNCNGCT	275	

	Qy	299	GGGGGCACTTCTTA	TGTGTGTGGCTGTGTCGGATATCGACGGGGAAAAGATTGTGTGCAA	358
	Db	276	GGGGCCACTTCTC	CACCGTCTGGCTCTGCTGGGANTTCNNCGCAAGCGCTTGTTGGGCC	335
	Qy	359	TGAAAGTTGTAA	AAAAGTCCACAGCATTTATAC - GGAGACAGCGCTTGGATGAATAAATTTG	417
	Db	336	TCAAATGGTGA	NAGTTCGGGGCATTTACCGGGAGACAGCTGTGGATGAATCAANCTC	395
	Qy	418	CT - CAAATGTG	TTTCGAGAAAGTGTATCCGAGTAGCCCAACAAAGA CATGGTGGTCCAGCT	476
	Db	396	CTGAATAATGT	COGGGACAGCACCCAGTGACCCCAAAAGAAAGACCATTTGTCCANCT	455
	Qy	477	CATTGACGACTT	CAAGATTTTCAGGCATGAATGGGATCATGTCTGCATGGTCTTTCGAAGT	536
	Db	456	CATTGTATGACT	TTCAGGATCTCANGAGTCAATGGGANTCCATGTGTGCATGGTGTGGANGT	515
	Qy	537	ACTTGGCCACCAT	CTCCTCAAGTGGATCATCAATCCAAC TATCAAGGCGCTCCCAAGTACG	596
	Db	516	GCTGGGGCACCA	NCCTCTC AAA TGATGATCNTCAANTCCAAC TACCANGGCGCTGCCCGTGCC	575
	Qy	597	TTGTGTGAAGAG	TATCATTTCCAGAGGTCCTTCAAGGGTTAGATTACTTTACACAGTAAAGTG	656
	Db	576	CTGCCTTNAANA	AACATCNTNWANGANGTGCTGCACNGCTGNANTACCCCAACCNANTTG	635
	Qy	657	CAAGATCAATTC	ATCATCTGACATAAAGCCGGAAAAATATCTTTGATGTGTGTGGATGA	710
	Db	636	CAANATNTTCC	ANCNGGAATCAANCCCCAAAACATCTTGTGTGTGTGGGGGA	689

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RESULT 11
US-09-016-434-808
; Sequence 808, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 808:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:

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2

Db 1340 AACGATGTGCAACCGCTGATATAGTCTCCAGAAAGTAATTCAGAGTGTCTCTCGGGA 1399
QY 1720 ACCCTCGGACATCTGGAGCAGCGGTGATGGCAATTTGAGCTGGCAACGGGAGATTAT 1779
Db 1400 GCTTCCGCTGATGCTGGAGTTTGGCTGTATCATTTTGAATTTGCTAACCGCGATTAC 1459
QY 1780 TTGTTTGAACCAATCTCTGGGAAGACTATTCAGAGACGAGACACATAGCCACATC 1839
Db 1460 CTTTTCGATCCCGAATGGAAATCTTATTTCTAAGGAGGATGACACATGCGCCAAAT 1519
QY 1840 ATAGAGCTGTAGCGAGTATTCAGGCACTTTGGCTCTATCTGGAATAATTCCTCGGAA 1899
Db 1520 ATTGAGTATTGTTTAATTCCTAAGCAATGGCACTTTCAGAAAGCACTCCCGGAT 1579
QY 1900 TTCTTCAATCGCAGAGAGAACTTCGCACATCACCAAGCTGAAGCCCTGGAGCCTCTTT 1959
Db 1580 TTATTTAAACCGTCGCGTGAATCCGAAATATTCATAAATTTGAAGTTTGGCCCTTAAAA 1639
QY 1960 GATGTACTTGTGAAAGTATGCTGGCCCAATGAAGATGCTGCACAGTTTACAGATTTC 2019
Db 1640 GATGTTTGGAGCAAAATACCAATTTTTCAGCCGAGTTGGCTCAACAAATATCAGACTTT 1699
QY 2020 CTGATCCGATGTTAGAAATGGTTCCAGAAACGAGCCTCAGCTGCGAATGCCCTTCG 2079
Db 1700 TTATCTCTATGTTATGTTTGTATCTGCAAGCAACCAATGCTGGTTACATGAGCAAT 1759
QY 2080 CATCCTTGGTGG 2091
Db 1760 TCTCCATGGTGG 1771

RESULT 14

US-09-248-796A-6406
; Sequence 6406, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR FILING DATE: 1998-02-13
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 6406
; LENGTH: 1731
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-6406

Query Match 7.4%; Score 155.4; DB 4; Length 1731;
Best Local Similarity 56.9%; Pred. No. 7.8e-32;
Matches 285; Conservative 0; Mismatches 216; Indels 0; Gaps 0;
QY 1592 ATGCAGATAAAATTAGAGTAAATAATTCGACCTGGGAATGCTGTTGGTGCATAAATAC 1651
Db 980 AATATGAAATTAATCTGTTAAATTTGCTGATTTGGTGAATGATGTTGACAAATCATC 1039
QY 1652 ACTTACGGAAGACATCCAGACGCGTCAGTACCGCTCCATAGAGGTTTAAATAGGAGCGG 1711
Db 1040 ATTTTACTGATGAATCCAAACAAAGACAATATCGAGCCCCCGAAATTTTAAATGGTTATT 1099
QY 1712 GGTACAGACCCCTCGGACATCTGGAGCAGCGGTGATGGCAATTTGAGCTGGCAACGG 1771
Db 1100 ATTGGGGTGCCTGAGTGAATTTATGTTGCTCAATTTGCCCTGTTTAAATATTGAATTAAC 1159
QY 1772 GAGATTATTGTTTGAACACATCTCTGGGGAAGACTATTCAGAGACGAGACCATAG 1831
Db 1160 GTGATTATCTATTGATCCTAGAGATGGTAAATCATATAAAAGATGATGATCATATTG 1219

QY 1832 CCCACATCATAGAGCTGTAGGCAAGTATTTCCAGGCACTTTTGCTCTATCTGGAATAATATT 1891
Db 1220 CCCAAATTTAGAAATTTGATTTGGACCAATTTTCTTAATCAAAATGTTAAAAAGAAATTTATG 1279
QY 1892 CTCGGGAATTTCTTAATCCAGAGGAGAACTCGGCACACATCACCAAGCTGAAGCCCTGGA 1951
Db 1280 CTCGAGAAATTTTCAATTCAGGTATGAATTAAGAAAGAAATCATGAAATTTAAACCTTTGGG 1339
QY 1952 GCCTCTTTGATGTACTTTGTGAAAAGTATGGCTGGCCCATGAAGATGCTGCACAGTTTA 2011
Db 1340 GGTTACAAGATGTAATTAATTTGAAAATATAAATTCCTTTTGAATGCTATTGAAATTA 1399
QY 2012 CAGATTTCTGATCCCGATGTTAGAAATGGTTCCAGAAAAACGAGCTCAGCTGGCGAAT 2071
Db 1400 GTGAATTTTATTTGCCAATGTTTGAATTTAAACACAGAAAGAGCTGATGCTGGAGGA 1459
QY 2072 GCCTTCGCGCATCTTGGTTGA 2092
Db 1460 TGTGTAATCATCTTGGTTAA 1480

RESULT 15

US-09-270-767-1008
; Sequence 1008, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1008
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1008

Query Match 5.6%; Score 117; DB 4; Length 569;
Best Local Similarity 67.3%; Pred. No. 9.9e-22;
Matches 165; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 1600 AAAATTTAGAGTAAAAATTTGCTGACCTGGGAATGCTTGTGGTGCATAAACAATTCACG 1659
Db 324 AACGTTGGGTAAAGATCGCCGACTTGGGGAACGCTCTACGACTACCATCACTTTACT 383
QY 1660 GAAGACATCCAGACGGTCAAGTACCGCTCCATAGAGTTTAAATAGAGGGGTACAGC 1719
Db 384 GAGGACATTCAGACTCGCCAGTATCGATCAATCGAGGTTCTTTTGGGAGCGCGTACAAT 443
QY 1720 ACCCTCGGACATCTGGAGACGCGTGTATGGCAATTTGAGCTGGCAACGGGAGATTAT 1779
Db 444 TATACCGCGACATCTGGAGCACAGCTGTTGGCTTCGAGCTGGCCACCGCGACTAC 503
QY 1780 TTGTTTGAACCACTTCTGGGAAGACTATTTCAGAGACGAGAACACACATAGCCACATC 1839
Db 504 CTGTTGACCCCTCACCGCGAGAGTCTTACAGTCGGGACGAGGACCACCTTGGCGCATATT 563
QY 1840 ATAGA 1844
Db 564 GTGGA 568

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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Sequence: 1 atgagctcccggaagtgc.....ggcatccttggtgaattct 2097

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Maximum Match 100%
Listing first 45 summaries

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12: gb.sy.*
13: gb.un.*
14: gb.vi.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2097	100.0	3253	6	AR265348	Sequence
2	2097	100.0	3253	6	AR566205	Sequence
3	2028.6	96.7	3157	9	BC035214	Homo sapi
4	2023.8	96.5	2577	9	BC068547	Homo sapi
5	2023.8	96.5	2791	6	AR077238	Sequence
6	2023.8	96.5	2791	6	BD107902	Protein k
7	2006.6	95.7	3708	6	C0715987	Sequence
8	1991.8	95.0	3745	6	AX429244	Sequence
9	1991.8	95.0	3745	6	AX566550	Sequence
10	1991.8	95.0	3745	9	HSU88866	Sequence
11	1814.6	86.5	3208	9	AY354201	Homo sapi
12	1562.6	79.3	2300	10	AB006036	Mus muscu
13	1357.6	79.0	3578	10	BC020178	Mus muscu
14	1552.2	78.8	4287	10	BC062941	Mus muscu
15	1284	61.2	2555	9	AK093420	Homo sapi
16	969.2	46.2	2326	9	AK090783	Homo sapi
17	833.6	39.8	183097	9	AC087358	Homo sapi
18	830	39.6	149318	9	AC091554	Homo sapi
19	828.4	39.5	183097	9	AC087358	Homo sapi

C	20	828.4	39.5	183360	2	AC0222525	AC022525 Homo sapi
	21	827.6	39.5	149318	9	AC091554	AC091554 Homo sapi
C	22	821.6	39.2	183360	9	AC022525	AC022525 Homo sapi
	23	723.4	34.5	917	10	MMU92456	U92456 Mus musculus
	24	677.4	32.3	984	6	CQ739202	CQ739202 Sequence
	25	631.4	30.1	4329	6	I26663	I26663 Sequence 1
	26	631.4	30.1	4296	6	AX410648	AX410648 Sequence
	27	631.4	30.1	4326	6	AX665648	AX665648 Sequence
	28	631.4	30.1	4326	9	HS009564	U09564 Human serin
	29	631.4	30.1	4760	9	HS0318054	U9318054 Homo sapi
	30	629.4	30.0	923	6	AR270140	AR270140 Sequence
	31	628.2	30.0	4252	6	CQ714961	CQ714961 Sequence
	32	628.2	30.0	4639	6	CQ414916	CQ414916 Sequence
	33	626.6	29.9	4296	9	HSN808814	BSX648663 Homo sapi
	34	626.6	29.9	4297	9	HSN808848	BSX648697 Homo sapi
	35	626.6	29.9	4388	9	BC038292	BC038292 Homo sapi
	36	621.6	29.6	2460	10	BC005707	BC005707 Mus muscu
	37	621.6	29.6	2485	10	BC050761	BC050761 Mus muscu
	38	620	29.6	2416	10	AB013290	AB013290 Mus muscu
	39	615.2	29.3	2469	10	MMAJ4115	AFJ224115 Mus muscu
	40	607.6	29.0	4071	10	AF446079	AF446079 Cricetulu
	41	565.4	27.0	984	5	CR385926	CR385926 Gallus ga
	42	563.8	26.9	2628	5	BC0056825	BC0056825 Danio rer
	43	486.8	23.2	90541	6	AR265349	AR265349 Sequence
	44	486.8	23.2	90541	6	AX6666207	AX6666207 Sequence
C	45	486.8	23.2	113033	9	AC005070	AC005070 Homo sapi

ALIGNMENTS

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RESULT 1
AR265348
LOCUS           AR265348             3253 bp      DNA              linear          PAT 10-APR-2003
DEFINITION     Sequence 1 from patent US 6492153.
ACCESSION      AR265348
VERSION        AR265348.1 GI:29693850
KEYWORDS
SOURCE         Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 3253)
AUTHORS       Abu-Thraideh,J., Gong,F., Ketchum,K.A., Di Francesco,V. and Beasley,B.M.
TITLE          Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
JOURNAL        Patent: US 6492153-A 1 10-DEC-2002;
FEATURES       Location/Qualifiers
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		Best Local Similarity	100.0%;	Pred. No. 0;		
		Matches 2097;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
Qy	1	ATGAGCTCCCGGAAAGCTGTGGCCATTTCAGGCCCGGAAAGCGGAGGCGCGAAAGAGAGAAA	60			
Db	91	ATGAGCTCCCGGAAAGCTGTGGCCATTTCAGGCCCGGAAAGCGGAGGCGCGAAAGAGAGAAA	150			
Qy	61	CATPCGAAAAGACCGGAGGCTTCAACGAAAGTCTCTTTTAGTTCTCTCTCTCCACCGCCA	120			
Db	151	CATPCGAAAAGACCGGAGGCTTCAACGAAAGTCTCTTTTAGTTCTCTCTCTCCACCGCCA	210			
Qy	121	CCACCAACCAACCGGCCACTTTGCGACAGACCCACACCCCGAGGCGAGGAGGAGATC	180			
Db	211	CCACCAACCAACCGGCCACTTTTGCCAGACCCCAACCCCGGAGCGCAGAGGAGGAGATC	270			
Qy	181	CTGGATCATGATGATGAGGACGAAGGAGCCCTTGGGACTACTGCAAAAGTGGATATCAT	240			
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ORIGIN

Query Match 100.0%; Score 2097; DB 6; Length 3253;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2097; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGCTCCGGAAGTGTGGCCATTTCAGGCCGGAAGCGGAGGCGGAAGAGAGAAA 60
DB |||||||
QY 91 ATGAGCTCCGGAAGTGTGGCCATTTCAGGCCGGAAGCGGAGGCGGAAGAGAGAAA 150
DB |||||||
QY 61 CATCCGAAAAAGCCGAGGCTCAACAGAAAGCTCTTTAGTTCTCTCTCTCTCCACCGCCA 120
DB |||||||
QY 151 CATCCGAAAAAGCCGAGGCTCAACAGAAAGCTCTTTAGTTCTCTCTCTCTCCACCGCCA 210
DB |||||||
QY 121 CCACCAACCAACCCGCCACTTTGGCCAGACCCCAACCCCGGAGCCAGAGGAGATC 180
DB |||||||
QY 211 CCACCAACCAACCCGCCACTTTGGCCAGACCCCAACCCCGGAGCCAGAGGAGATC 270
DB |||||||
QY 181 CTGGGATCAGATGATGAGGAGCAAGAGACCTTGGGACTCTGCAAGGTGATATCAT 240
DB |||||||
QY 271 CTGGGATCAGATGATGAGGAGCAAGAGACCTTGGGACTCTGCAAGGTGATATCAT 330
DB |||||||
QY 241 CCAGTGAAATTTGGAGACCTTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATG 300
DB |||||||
QY 331 CCAGTGAAATTTGGAGACCTTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATG 390
DB |||||||
QY 301 GGGCACTTCTCTACTGTCTGGCTGTGGGATATGCAAGGGAAGATTTGTTGCAATG 360
DB |||||||
QY 391 GGGCACTTCTCTACTGTCTGGCTGTGGGATATGCAAGGGAAGATTTGTTGCAATG 450
DB |||||||
QY 361 AAAGTTGTAAGAGTCCAGACATATACGGAGACAGCTTGGATGGAATAAATTTGCTC 420
DB |||||||
QY 451 AAAGTTGTAAGAGTCCAGACATATACGGAGACAGCTTGGATGGAATAAATTTGCTC 510
DB |||||||
QY 421 AAATGTGTTGGAAGAGTGCATCCAGTGACCCAAACAAAGACATGGTGTCCAGCTCAT 480
DB |||||||
QY 511 AAATGTGTTGGAAGAGTGCATCCAGTGACCCAAACAAAGACATGGTGTCCAGCTCAT 570
DB |||||||
QY 481 GAGCACTTCAAGATTTGAGGATGATGATGATGATGATGATGATGATGATGATGATG 540
DB |||||||
QY 571 GAGCACTTCAAGATTTGAGGATGATGATGATGATGATGATGATGATGATGATGATG 630
DB |||||||
QY 541 GGCACCATCTCTCTAAGTGGATCATCAATCCAACTCAAGGCTCCAGTACGTTGT 600
DB |||||||
QY 631 GGCACCATCTCTCTAAGTGGATCATCAATCCAACTCAAGGCTCCAGTACGTTGT 690
DB |||||||
QY 601 GTGAAGAGTATCATTCGACAGGTCCTTCAAGGTTAGATTCTTACAGTAAGTCCAG 660
DB |||||||
QY 691 GTGAAGAGTATCATTCGACAGGTCCTTCAAGGTTAGATTCTTACAGTAAGTCCAG 750
DB |||||||
QY 661 ATCATTTACTGACATAAAGCGGAAAAATATCTTGATGTGTGGATGATGATGATG 720
DB |||||||
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DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: <http://www.shgc.stanford.edu>
 Contact: (Dickson, Mark) mcd@paxil.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 167 Row: 1 Column: 18
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4507220.

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Location/Qualifiers

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Query Match

96.5%; Score 2023.8; DB 9; Length 2577;

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AR077238
LOCUS
DEFINITION
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VERSION

Sequence 8 from patent US 5962232.
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GI:10003984

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LOCUS CQ715987 3708 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 1921 from Patent WO02068579.
ACCESSION CQ715987
VERSION CQ715987.1 GI:42276844
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof

AUTHORS

PE Corporation (NY) (US)

JOURNAL

Patent: WO 02068579-A 1921 06-SEP-2002;

FEATURES

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Matches 2031; Conservative 0; Mismatches 4; Indels 2; Gaps 2;			
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Db	1522	CCGAGATTTTCCACCTCGTTGTTCTCTGGATCCTTAGAACCTCTGGCTCGGCTCTGT	1581
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RESULT 8
AX429244
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS

AX429244
Sequence 21 from Patent EPI201765.
AX429244
AX429244.1
GI:21540552

3745 bp
DNA
linear

PAT 21-JUN-2002

SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	artificial sequences.
AUTHORS	1
TITLE	Schubart, D., Habenberger, P., Stein-Gerlach, M. and Bevec, D.
JOURNAL	Cellular kinases involved in cytomegalovirus infection and their inhibition
Patent:	EP 1201765-A 21 02-MAY-2002;
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LOCUS AX666550 3745 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 3 from Patent WO02094796.
ACCESSION AX666550
VERSION AX666550.1 GI:29291032
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
REFERENCE
AUTHORS Pato,J., Keri,G., Oerfi,L., Waczek,F., Horvath,Z., Banhegyi,P.,
Szabadkai,I., Marosfalvi,J., Hegymegi-Barakonyi,B., sz kelyhidi,Z.,
Greff,Z., Choidas,A., Bacher,G., Daub,H., Obert,S., Kurtenbach,A.
and Habenberger,P.
TITLE Benzo[gl]quinoxaline derivatives as effective compounds against
infectious diseases
JOURNAL Patent: WO 02094796-A 3 28-NOV-2002;
Axixma Pharmaceuticals Aktiengesellschaft (DE)
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Matches 2022; Conservative 0; Mismatches 7; Indels 6; Gaps 2;
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DEFINITION	Homo sapiens SFRS protein kinase 2 isoform c (SRPK2) mRNA, complete cds, alternatively spliced.		
ACCESSION	AY354201		
VERSION	AY354201.1	GI:34329349	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 3028)		
TITLE	Sha, J.H., Zhou, Z.M. and Li, J.M.		
JOURNAL	Direct Submission Submitted (29-JUL-2003) Key Lab of Reproductive Medicine, Nanjing Medical University, 140 Han Zhong Road, Nanjing, Jiangsu 210029, China		
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Qy	183	GGGATCAGATGATGAGAGCAGAGACCTTCGCGACTACTGCAAAAGGTGGATATCATCC	242
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AB06036.1 GI:2723281
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 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (sites)
 Kuroyanagi,N., Onogi,H., Wakabayashi,T. and Hagiwara,M.
 Novel SR-protein-specific kinase,SRPK2,diseassembles nuclear
 speckles
 Biochem. Biophys. Res. Commun. (1998) In press
 2 (bases 1 to 2300)
 Hagiwara,M.
 Direct Submission
 Submitted (25-JUL-1997) Masatoshi Hagiwara, Tokyo Medical and
 Dental University Medical Research Institute, Department of
 Endocrinology; Yushima, Bunkyo-Ku, Tokyo 113, Japan
 (E-mail:m.hagiwara.end@mri.tmd.ac.jp, Tel:03-5803-5836,
 Fax:03-5803-5836)
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 QY 123 ACCACACACCGCCACCTTTCGCCAGACCCACACCCCGGAGCCAGAGGAGGAGATCCT 182
 Db 90 ACCGCCACCAACAC-----TGCAGACCCCGGCCCCAGAGCCAGAGGAGGATCT 143
 QY 183 GGGATCAGATGATGAGGACCAAGAGACCCCTGGGACTACTCGCAAGTGGATATCATCC 242
 Db 144 GGGGTTCAGATGATGAGGACGAGGACCCCGCAGATTACTGCAAGSTGGCTATCATCC 203
 QY 243 AGTGAAAAATTGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGGG 302
 Db 204 AGTGAAAAATTGGAGATCTCTTCAATGGTGCATATCATGTCATTAGAAAGCTAGGATGGG 263
 QY 303 GCACCTTCTTACTGTCTGGCTGTGCTGGGATATGCAGGGGAAAAGATTGTTGCAATGAA 362
 Db 264 GCACCTTCTTACTGTATGGCTGTGCTGGGATATGCAAGGGAAAAGATTGTTGCAATGAA 323
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Matches 1825; Conservative 0; Mismatches 189; Indels 24; Gaps 3;			
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Ds	134	TTCAAAAGGCGGAGCCTCAACGAAGCTCCTTTAGTTCCTCCTCCACCGCCACC	193
Qy	123	ACCACACACCGCCACCTTTGCCAGAGCCCCACACCCCGGAGCCAGAGGAGATCCT	182
Ds	194	ACCGCACACAC-----TGCAGACCCCGACCCCGAGCCAGAGGAGGATCT	247
Qy	183	GGATCAGATGATGAGGAGAGAGACCTTGGGAGCTACTTGCAGAGTGATATCATCC	242
Ds	248	GGGTCAGATGATGAGGAGAGAGACCTTGGGAGCTACTTGCAGAGTGATATCATCC	307
Qy	243	AGTGAATTTGGAGACCTCTCAATGGCGGCTATCATCTTATGAGAGCTTGGATGGG	302
Ds	308	AGTGAATTTGGAGATCTCTCAATGGCTCGATATCATCTTATGAGAGCTAGATGGG	367
Qy	303	GCATCTCTACTGTCTGCTGTGGATATGAGGGGAAAGATTTGTGCAATGAA	362
Ds	368	GCATCTCTACTGTATGGCTGTGGATATGCAAGGAAAGATTTGTGCAATGAA	427
Qy	363	AGTTGTAAGAGTGCAGAGATTTACGGAGACAGCCTTGGATGAAATTAATTTCTCAA	422
Ds	428	AGTTGTAAGAGTGCAGAGATTTACAGAGACAGCCTTGGATGAAATTAATTTCTCAA	487
Qy	423	ATGTCTTCGAGAGATGATCCAGTGACCCAAACAAAGACATGGTGGTCCAGTCTATGA	482
Ds	488	ATGCGTTCGAGAGATGATCCAGTGACCCAAACAAAGACATGGTGGTCCAGTCTATGA	547
Qy	483	CGACTTCAAGATTTTCAGGATCAATGGGATACATGTCTGCATGTCTTTCGAAGTACTGG	542
Ds	548	TCAGCTTCAAGATCTCAGGATCAATGGGATACATGTCTGCATGTCTTTCGAAGTACTGG	607
Qy	543	CCACCATCTCTCAAGTGGATCATCAATCCAACTATCAGGCCCTCCAGTACGTTGTGT	602
Ds	608	TCACCATCTCTCAAGTGGATCATCAATCCAACTATCAGGCCCTCCAGTACGTTGTGT	667
Qy	603	GAAGAGTATCATTTCAGACAGTCTTCAAGGTTTATGATTACTTACACAGTAAGTCAAGAT	662
Ds	668	GAAGAGTATCATTTCAGACAGTCTTCAAGGTTTATGATTACTTACACAGTAAGTCAAGAT	727
Qy	663	CATTCTACTGACATAAAGCCGGAATAATCTTGTGTGTGGATGATGCAATATGTGAG	722
Ds	728	AATTTCACCGACATAAAGCCGGAATAATCTTGTGTGTGGATGATGCAATATGTGAG	787
Qy	723	AAGATGGCAGTGGAGCCACTGATGGGAGAGAGAGTGTCTCTCTCTTTCAGGTC	782
Ds	788	AAGATGGCAGGCGAAGCCAGGAGTGGCAGAAAGCAGGTGTCTCTCTCTCTCTCTCT	847
Qy	783	TGCAGTGTAGTGGCTCCACAGCAGAAACCTATAGGAAATAATCTTAAAAACAAAAAGAA	842
Ds	848	TGCAGTGTAGTGGCTCCACAGCAGAAACCTATAGGAAATAATCTTAAAAACAAAAAGAA	907
Qy	843	AAAACTGAAAAAGAAACAGAGAGGCGAGTGTGATTTATTTGGAAGCGCTCGAGAGAT	902
Ds	908	AAAGCTGAAAAAGAAACAGAGAGGCGAGTGTGATTTATTTGGAAGCGCTCGAGAGAT	967
Qy	903	AGAGAAATTTGGACGAGAGCTGAAAGGAAATAATAGAGAAACATCACTTCAGTCTC	962
Ds	968	TGAGGAATTTGGACGAGAGCTGAAAGGAAATAATAGAGAAACATCACTTCGAGAG	1027
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Ds	1028	AGCTTCGGGGACGACGAGATGGAGATACAGTCCAGCCGAGGTGACACTGAAGACCCGA	1087
Qy	1020	ATTAGAGGAGCGGCTGAGCAGAGACTGCAAAAGGACAAATGGTGAAGCTGAGGACAGGA	1079
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RESULT 14
BC062941
LOCUS
DEFINITION
ACCESSION

BC062941
Mus musculus serine/arginine-rich protein specific kinase 2, mRNA
(cdna clone IMAGE:6842723), complete cds.
4287 bp
linear
ROD 11-DEC-2003

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Qy	1200	TGGCCCATCTTCACTGGAGCAGCAACTGGACGATGAGATGATGATGATGATGATGATGAT	1259
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Ds	1438	-----CAGAGTTTCCACACCGTGTGTCTTGGGCCCTTGAACCTCTGAGCCTGCGGCTC	1492
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Ds	1973	ACTGCGGACACATCAACAGCTGAGCCCTGAGGCTCTTTGATGATCTTTGTTGGAAGATTA	2032
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
BC062941.1 GI:38566029
Mus musculus (house mouse)
Mus musculus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4287)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
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Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krywinski, M.I., Skalska, U., Smalish, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 4287)
Strausberg, R.
Direct Submission
Submitted (26-NOV-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapps@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
Fisher, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
Schetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J.,
Casavant, T., Soares, M.B.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: Plate: Row: Column: 0
This clone has the following problem: The cds is short compared to
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Best Local Similarity 88.8%; Pred. No. 0;
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QY 136 CCACCTTTCCAGACCCACACCCCGAGGAGGAGGAGGAGATCTGGGATCAGATGAT 195
Db 255 C-----TGCCAGACCCCGACCCCGAGGAGGAGGAGGAGATCTGGGATCAGATGAT 308

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Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuko, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project

JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 2565)
AUTHORS	Isogai, T. and Yamamoto, J.
TITLE	Direct Submission
JOURNAL	Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
COMMENT	(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

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	Matches 1284;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Job time : 8685.01 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
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(without alignments)
12141.282 Million cell updates/sec

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Perfect score: 3253
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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DEFINITION full-length cDNA clone CS0DN003YA14 of Adult brain of Homo sapiens (human).
ACCESSION CR624570
VERSION CR624570.1 GI:50505377
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue
REFERENCE 2 (bases 1 to 1765)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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CS0DN003YA14 5-PRIME, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
BX463511.2 GI:47056867
Homo sapiens (human)

REFERENCE
AUTHORS
JOURNAL
COMMENT
1 (bases 1 to 995)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced gi:31027556.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and ScaRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4027.r
For more information about this cluster, see

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QY	2539	ATATTTTAGCTGAGTACTATATAATTTACAATTTTACAATTTTACAATTTTACAATTTTACA	2598
DB	1021	CATATTTTAGCTGAGTACTATATAATTTACAATTTTACAATTTTACAATTTTACA--GTTGGA	1078
QY	2599	AGAAATAGCAAGGAAATGTACAATTTTATCTTCGCAAGGAGGACATCATTCCTGTAT	2658
DB	1079	AGAAA--GAGCAAGGAAATGTACAATTTTATCTTCGCAAGGAGGAAATCATTCCTGTAT	1136
QY	2659	TATAGT 2664	
DB	1137	TATAGT 1142	
RESULT 5			
BX384358			
LOCUS			
DEFINITION		BX384358 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens	
ACCESSION		BX384358	
VERSION		BX384358.2	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	
TITLE		Full-length cDNA libraries and normalization	
JOURNAL		Unpublished (2001)	
COMMENT		On May 8, 2003 this sequence version replaced gi:30451233.	
		Contact: Genoscope	
		Genoscope - Centre National de Sequencage	
		BP 191 91006 EVRY cedex - France	
		Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr	
		1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime	
		end enriched, double-strand cDNA was digested with Not I and cloned	
		into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library	
		was normalized. Library was constructed by life technologies, a	
		division of Invitrogen. This sequence belongs to sequence cluster	
		4027.r	
		For more information about this cluster, see	
		http://www.genoscope.cns.fr/cdna?8=CS0DK009AB06QP1&c=4027.r.	
FEATURES		Location/Qualifiers	
source		1..1001	

Qy	1453	AAAAATCCCGAGTACAGTTC	CGAGATTTCC	CACTCGTCTCTGGATCCTTAGAA	900
Db	841	AAAAATCCCGAGTACAGTTC	CGAGATTTCC	CACTCGTCTCTGGATCCTTAGAA	900
Qy	1513	CTGTGGCTCGCGCTCTGTGCTTTCTGAGGGATCACCACTTACTGAGCAAGAGGAGGC	1572		
Db	901	CTGTGGCTCGCGG-TCTGTGCVTTCTGAGGGAT-MCCMCTTACTGRC-AGRGGAGAGC	957		
Qy	1573	AGTCCATCCCATGACAGAGCA	1594		
Db	958	AGTCATCCCGACAGAAACCA	979		

ORIGIN

Query Match	28.5%;	Score 927.6;	DB 5;	Length 1001;
Best Local Similarity	97.8%;	Pred.No. 4.2e-198;		
Matches 960;	Conservative 10;	Mismatches 9;	Indels 3;	Gaps 3;
Qy	613	ATGGTCTTTCGAAGTACTTGGCCACCACATCTCCTCAAGTGGATCATCAAAATCCAACTATCAAA	672	
Dd	1	ATGGTCTTTCGAAGTACTTGGCCACCACATCTCCTCAAGTGGATCATCAAAATCCAACTATCAAA	60	
Qy	673	GGCCTCCAGTAGCTTGTGTGAAGAGTATCATTTGCACAGGTCCCTCAAGGGTGTAGATTAC	732	
Dd	61	GGCCTCCAGTAGCTTGTGTGAAGAGTATCATTTGCACAGGTCCCTCAAGGGTGTAGATTAC	120	
Qy	733	TTACACAGTAACTGCAAGATCATTTCACTCTGCATATAAAGCCGGAATAATCTTGTATGTGT	792	
Dd	121	TTACACAGTAACTGCAAGATCATTTCACTCTGCATATAAAGCCGGAATAATCTTGTATGTGT	180	
Qy	793	GTGGATGATGCATATGTGAGAAGATGGCAGCTGAGGCCACCTGAGTGGCAGAAACGAGGT	852	
Dd	181	GTGGATGATGCATATGTGAGAAGATGGCAGCTGAGGCCACCTGAGTGGCAGAAACGAGGT	240	
Qy	853	GCTCCTCTCCTTTCAGGGTCTCGAGTGAGTACGGCTCCACAGCAGAAAACTATAGAAAA	912	
Dd	241	GCTCCTCTCCTTTCAGGGTCTCGAGTGAGTACGGCTCCACAGCAGAAAACTATAGAAAA	300	
Qy	913	ATATCTTAAAAACAAAAAGAAAAAACTGTAAAAAGAAAAGAAAGAGCGAGCTGAGTTATTGT	972	
Dd	301	ATATCTTAAAAACAAAAAGAAAAAACTGTAAAAAGAAAAGAAAGAGCGAGCTGAGTTATTGT	360	
Qy	973	GAGAAGCGCTGCAGAGATAGAAAGATTTGGACGAGAGAGCTGTAAAAGGAAAAATAATAGAA	1032	
Dd	361	GAGAAGCGCTGCAGAGATAGAAAGATTTGGACGAGAGAGCTGTAAAAGGAAAAATAATAGAA	420	
Qy	1033	GAAAAACATCACCTCAGCTGCACCTTCCATATGACCGAGATGGCGAATACTGCCACAGGGTG	1092	
Dd	421	GAAAAACATCACCTCAGCTGCACCTTCCATATGACCGAGATGGCGAATACTGCCACAGGGTG	480	
Qy	1093	AAACTTAAAAACACAGATTAGAGGAGCGGCTGAGGCAGAGACTGCAAGAGCAATGGT	1152	
Dd	481	AAACTTAAAAACACAGATTAGAGGAGCGGCTGAGGCAGAGACTGCAAGAGCAATGGT	540	
Qy	1153	GAAGCTGAGCACACAGGAAGAGAAGAGATGCTTGAGAAAGAAAAACATTTGAAAAAGATGAA	1212	
Dd	541	GAAGCTGAGCACACAGGAAGAGAAGAGATGCTTGAGAAAGAAAAACATTTGAAAAAGATGAA	600	
Qy	1213	GATGATGTAGATCAGGAACTTGGCAACATAGACCTTACGTGGATAGAAATCACCTTAAACC	1272	
Dd	601	GATGATGTAGATCAGGAACTTGGCAACATAGACCTTACGTGGATAGAAATCACCTTAAACC	660	
Qy	1273	AATGGCCATATTGAGATGGCCCATCTCACTGGAGCAGCAACTGGACGATGAAGATGAT	1332	
Dd	661	AATGGCCATATTGAGATGGCCCATCTCACTGGAGCAGCAACTGGACGATGAAGATGAT	720	
Qy	1333	GATCAAGAAGACTGCCCAAAATCCTTGAGGAATATTAATCTTGATAGGCCAAATTCGAGAAAGT	1392	
Dd	721	GATCAAGAAGACTGCCCAAAATCCTTGAGGAATATTAATCTTGATAGGCCAAATTCGAGAAAGT	780	
Qy	1393	GATTACACATATAGAGCTCCTATGAACAATTTCAATGGTGAATTTGCCAAATTCGACGACAT	1452	
Dd	781	GATTACACATATAGAGCTCCTATGAAMAATTTCAATGGTGAATTTGCCAAATTCGACGACAT	840	

RESULT	6
LOCUS	EST 05-MAY-2004
DEFINITION	Homo sapiens cdna clone
ACCESSION	EX463510
VERSION	BX463510 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone CS0DN003YA14 3-PRIME, mRNA sequence.
KEYWORDS	
SOURCE	GI:47055934
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1025) Li,W.B., Gruber,C., Jesse,J., Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On May 22, 2003, this sequence version replaced gi:31025523.
AUTHORS	
TITLE	
JOURNAL	
COUNTRY	

On May 22nd, 2008, we sequenced the following:

Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 131 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

The first strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 4027.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CS0DN003BA07NP1&c=4027.r>.

FEATURES source

FEATURES	SOURCE
location/sequence	i. 1025
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/clone="CS0DN003YA14"
	/tissue_type="ADULT BRAIN"
	/dev_stage="adult"
	/clone_lib="Homo sapiens ADULT BRAIN"
	/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

[illegible]

FEATURES	Location/Qualifiers	
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	/organism="Mus musculus"	
	/mol_type="mRNA"	
	/strain="C57BL/6J"	
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	/db_xref="taxon:10090"	
	/clone="A630008K11"	
	/tissue_type="thymus"	
	/clone_lib="RIKEN full-length enriched mouse cDNA library"	
CDS	28..591	
	/note="unnamed protein product; putative serine/arginine-rich protein specific kinase 2 (MGD) [GI:1201408, GB NM_009274, evidence: BLASTN, 99%, match=921]"	
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	/protein_id="BAC30942.1"	
	/db_xref="GI:26334483"	
	/translation="MAAKTRADILVNPDLPRNADKIRVKIADLGNACVHKHFTEDI QTRQSRLEVLIGAGTSPADIWSTACNAFELATGDYLFEPHSGEDYSRDEHDIAHII ELIGSPIRHFALSGYSREFFNRRELRIHTKLPWSLFDVLVEKIGWPHEDAAQFTD FLIPLEWVPEKRSAGBCLRHPWLNS"	
ORIGIN	Query Match	
	Best Local Similarity 26.1%; Score 847.6; DB 3; Length 1486;	
	Matches 954; Conservative 0; Mismatches 74; Indels 12; Gaps 5;	
	QY	1632 AGCAAAACCCGGGAGCTGACTTGTGTGTAATCCCTCGATCCGCGAATGCAGATAA 1691
	DB	33 AGCAAAACCCGGCGGCTGACCTGTGTGTAACCTCTGGATCCAGGAATGCAGATAA 92
	QY	1692 AATTAGATAAATTTGCTGACCTGGGAAATGCTTGTGGTGCATATAACACTTCAACGA 1751
	DB	93 AATTAGATAAATTTGCTGACCTGGGAAATGCTTGTGGTGCATATAACACTTCAACGA 152
	QY	1752 AGACATCCAGACGCTCAGTACCGCTCCATAGAGTGTAAATAGGACGGGTACAGCAC 1811
	DB	153 GGATATCCAGACAGCTCAGTATAGTTCATAGAGTGTAAATAGGACGGGTACAGCAC 212
	QY	1812 CCCTGGCGACATCTGGAGCAGCGCGTGTATGGCAATTTGAGCTGGCAACGGGAGATTATTT 1871
DB	213 ACCTGCAGACATTTGGAGTACAGCTTGCATGTCATTTGAGCTCGCCACAGAGACTATTT 272	
QY	1872 GTTTGAACACATTTCTGGGGAAGACTATTCAGAGCAGACACACATAGCCACATCAT 1931	
DB	273 GTTTCGAACCGCATTTCTGGGGAAGACTATTCAGAGATGAAGACACATAGCCACATCAT 332	
QY	1932 AGAGCTGCTAGGAGATTTCCAAAGGACATTTGCTCTATCTGGAATAATTTCTCGGGAATT 1991	
DB	333 AGAGCTGCTAGGAGATTTCCAAAGGACATTTGCTCTGCTGGAATAATTTCTCGGGAATT 392	
QY	1992 CTTCAATTCGACAGAGGAGAACTGCGACATCATCAACAGCTGAAGCCCTGGAGCCTCTTTGA 2051	
DB	393 CTTCAATTCGACAGAGGAGAACTGCGGACATCATCAACAGCTGAAGCCCTGGAGCCTCTTTGA 452	
QY	2052 TGTACTTGTGGAAGATGCTGGCGCCCATGAAGATGCTGCACAGTTTACAGATTTCCT 2111	
DB	453 TGTACTTGTGGAAGATGCTGGCGCCCATGAAGATGCTGCACATTTTACAGATTTCCT 512	
QY	2112 GATCCCGATGTTAGAAATGTTCCAGAAAAACAGAGCTCAGCTGGCGAATGCCCTTCGGCA 2171	
DB	513 GATCCCAATGTTAGAGATGTTCCAGAAAAACAGAGCTCAGCTGGCGAATGCCCTTCGACA 572	
QY	2172 TCCTTGGTGAATTTCTAGCAATTTACCAATATTCGATCTGAGTGCAGCAATGCTTC 2230	
DB	573 TCCTTGGTGAATTTCTAGCAGATTTACAAATATAGCATTTCTGAGTAGCAAAATTTCTC 632	
QY	2231 CCAGTACATTGGACCTAAACGGTGACTCTCATTTCTTTTAAACAGGATTACAGTGAGCTGGC 2290	
DB	633 CCAGTACATTGGACCTACACAGTGGCTCTCATTTTAAACAGGATTACAGTGAGCTGGC 692	

QY	2291	TTCATCTCAGACCTTTATTTTGTCTTTGAGTACTGTTTGTGACATTTTGTCTTTTGTG 2350
DB	693	TCACACCTCAGACCTTTGTAGTCTTTGAGTACTGTTTGTGACACTTTGCTTCTCTGTG 752
QY	2351	CACCTGTATCTCGGGAAGGTTAGTCTTTTGTCTTCTGAGTACTGTTTGTGACACTTTT 2410
DB	753	CACCATGTTCTCGGGAAGGCTGGTC-TTTGTCTTCCAGCTAAAGTAGTTTACTGGCCATT 811
QY	2411	TCCTTGGAAACAAATACATGCTCTTAAGCATTTTCTTGTGTTGTTGTTGTTGTTGTTG 2470
DB	812	TCCTTGGAAACAAATACATGCTCTTAAGCATTTTCTTGTGTTGTTGTTGTTGTTGTTG 871
QY	2471	GTC-----ATTTTGTGAATGAAATATCTTTCCCTTTGTTGTTTGGCAGGTTTGTGA 2524
DB	872	GTCCTTTTGTGTTTGTGAAACGAAATATCTTTCCCTTTGTTGTTTGGCAGGTTTGTGA 931
QY	2525	ACTATTTATGAAGAAATATTTTGTAGCTGAGTACTATATAATTTACAATCTTTAAGAAAT 2584
DB	932	ACTATTTATGAAGACATATTTTGTAGCTGAGTATATATAATTTACAATCTTTAAGAAAT 991
QY	2585	CAAGTTGGGAACCAAGAAAAATAGCAAGGGAATGTACAAATTTTATCTTCTGGCAAGGGA 2644
DB	992	CA--GTTGGAAACCAAGAA--GAGCAAGGAATGTACAAATTTTATCTGCTGCGCAAGGGA 1047
QY	2645	CATCATTCCTGTATTATAGT 2664
DB	1048	AATCATTCCTGTATTATAGT 1067

RESULT 8

BX423897/c

LOCUS

DEFINITION BX423897 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone

ACCESSION CS0DN003YA14 3-PRIME, mRNA sequence.

VERSION BX423897.2 GI:46926197

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1014)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On May 13, 2003 this sequence version replaced gi:30638759.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 4027.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna/s=C51AN001ZE08NP1&c=4027.r.

Location/Qualifiers

1..1014

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DN003YA14"

/tissue_type="ADULT BRAIN"

/dev_stage="adult"

/clone_lib="Homo sapiens ADULT BRAIN"

/note="organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

FEATURES

source

ORIGIN


```
Query Match      25.4%; Score 826.8; DB 5; Length 1014;
Best Local Similarity 91.5%; Pred. No. 2.3e-175;
Matches 922; Conservative 34; Mismatches 39; Indels 13; Gaps 8;

QY 1657 TTGGTGAATCCCTGGATCCGCGGAATGCAGATAAAATAGAGTAAATAATGCTGACCTG 1716
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Db 997 KXTGGAAVCCCTGGACCCGCGRADBMRAAAAATAGAKATAAA--TKSCTACCTT 940

QY 1717 GGAATGCTTTGGTGATAAACATCTTACGGAAGACATCCAGACGGCTCAGTACCGC 1776
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Db 939 GRAAATGCTTG-TGGGTGCAAAACATCTTACGGAAGACACCCARACGCKWAGTACCGC 881

QY 1777 TCATAGAGTTTATAGAGCGGGTACAGACCCCTGCGACATCTGGAGCAGGC- 1835
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Db 880 TCMATAGA-GTTTTATAGAGC-GGGTACAGACCCCTGCGACATCTGGAGCAGGCT 823

QY 1836 GTGTATGGCATTTGAGCTGGCAACGGGAGATTA-TTTGTTTGAACACACATCTTGGGGAAG 1894
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Db 822 GTGTATGGCATTTGRCCTGGCAACGGGAGATTA-TTTGTTTGAACACATCTTGGGGAAG 763

QY 1895 ACTATCCAGAGACGAGACCATAGAGCCACATCATAGAGTGTCTAGGAGTATTCCAA 1954
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Db 762 ACTATCCAGAGACGAGACCATAGAGCCACATCATAGAGTGTCTAGGAGTATTCCAA 703

QY 1955 GGCACCTTCTCTATCTGGAATATCTCGGAATCTTCTCAATCCAGAGGAGACTGC 2014
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Db 702 GGCACCTTCTCTATCTGGAATATCTCGGAATCTTCTCAATCCAGAGGAGACTGC 643

QY 2015 GACACATCAACAGCTGAAGCCCTGGAGCTCTTTGATGTACTTGTGGAAAAGTAGTGGCT 2074
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Db 642 GACACATCAACAGCTGAAGCCCTGGAGCTCTTTGATGTACTTGTGGAAAAGTAGTGGCT 583

QY 2075 GGGCCCATGAAGTGTGCACAGTTTACAGATTTCTCTGATCCGATGTTAGAAATGGTTC 2134
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Db 582 GGGCCCATGAAGTGTGCACAGTTTACAGATTTCTCTGATCCGATGTTAGAAATGGTTC 523

QY 2135 CAGAAAAACGAGCTCAGCTGGGGAATGCTTGGCATCTTGGTGAATTTCTAGCAAA 2194
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Db 522 CAGAAAAACGAGCTCAGCTGGGGAATGCTTGGCATCTTGGTGAATTTCTAGCAAA 466

QY 2195 TTCTACCAATATTGCAATCTGAGTACGAAATGTTCCAGTACATTTGGACCTTAAACGGTG 2254
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Db 405 ACTCTCAATCTTTAAGAGTATCAAGTGAAGTGGCTTCACTCTCAGACCTTTATTTTCG 346

QY 2315 TTTGAGTACTGTTGTTGACATTTGCTTTTGTGACATGTGATCTCGGGAAGGGTAG 2374
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Db 345 TTTGAGTACTGTTGTTGACATTTGCTTTTGTGACATGTGATCTCGGGAAGGGTAG 286

QY 2375 TCTTTTGTCTCAGCTAAGTAGTTTACTGACCAATTTTCTTGGAAACAAATACATGTCT 2434
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Db 285 TCTTTTGTCTCAGCTAAGTAGTTTACTGACCAATTTTCTTGGAAACAAATACATGTCT 226

QY 2435 CTAAGCATTTGTTCTTTGTGTGTGACATTTCAAATGTCAATTTTTTGAATGAAAATAC 2494
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Db 225 CTAAGCATTTGTTCTTTGTGTGTGACATTTCAAATGTCAATTTTTTGAATGAAAATAC 166

QY 2495 TTTCCCTTTGTTTGGCAGGTTTGTAACTATTATTTATGAGAAATATTTTGTAGTGAAT 2554
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Db 165 TTTCCCTTTGTTTGGCAGGTTTGTAACTATTATTTATGAGAAATATTTTGTAGTGAAT 106

QY 2555 ACTATATAATTTACATCTTACAAATTTCAAGTTGGGAACCAAGAAATAGCAGGA 2614
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Db 105 ACTATATAATTTACATCTTACAAATTTCAAGTTGGGAACCAAGAAATAGCAGGA 49

QY 2615 AATGTACAAATTTTATCTTGGCAAGGAGCATCATCTCTGTTATATA 2662
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Db 48 NNGKAAATYNYMTCSYTVGYAGGGGTACATCGTTCTCTGTATATA 1
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RESULT 9

AL045362/c

LOCUS

DEFINITION DKF2p434C115_81_434 (synonym: htes3) Homo sapiens cDNA clone

DKF2p434C115_3', mRNA sequence.

ACCESSION

AL045362

VERSION

AL045362.1 GI:5433514

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 836)

REFERENCE

Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and

AUTHORS

Wiemann, S.

TITLE

EST (Duesterhoeft, et al.)

JOURNAL

Unpublished (1999)

COMMENT

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 3' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;

sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing

consortium of the German Genome Project.

r1 sequence also available.

This clone (DKF2p434C115) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1..836

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DKF2p434C115"

/tissue_type="testis"

/dev_stage="adult"

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/clone_lib="434 (synonym: htes3)"

/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

ORIGIN

Query Match 24.2%; Score 786; DB 1; Length 836;
Best Local Similarity 99.8%; Pred. No. 3.6e-166;
Matches 808; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

QY 1637 AAACCCGGCAGCTGACCTTTGTTGGTGAATCCCTGGATCCGCGAATGAGATAAAATTA 1696
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Db 836 AAACCCGGCAGCTGACCTTTGTTGGTGAATCCCTGGATCCGCGAATGAGATAAAATTA 777
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QY 1697 GAGTAAAAATTCCTGACCTGGGAAATGCTTTGTTGGTGCATAAACAATTCACGGAAGACA 1756
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QY 1757 TCCAGACGGTCAGTACCGCT-CCATAGAGTTTAAATAGGAGCGGGGTACAGACCCCT 1815
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Db 716 TCCAGACGGTCAGTACCGCTCCCATAGAGTTTAAATAGGAGCGGGGTACAGACCCCT 657
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QY 1816 GCGGACATCTGGAGCAGCGGTGATGCAATTTGAGCTGGCAACCGGAGATTTTGTGTT 1875
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Db 656 GCGGACATCTGGAGCAGCGGTGATGCAATTTGAGCTGGCAACCGGAGATTTTGTGTT 597
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QY 1876 GAAACACATTTCTGGGGAAGACTATTCCAGAGACGAAGACACATAGCCACATCATAGAG 1935
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 596 GAAACACATTTCTGGGGAAGACTATTCCAGAGACGAAGACACATAGCCACATCATAGAG 537
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1936 CTGTAGGAGTATT-CCAAGGCACTTTGCTCTATCTGGAATAATTTCTCGGAATTCCT 1994
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 536 CTGTAGGAGTATTCCCAAGGCACTTTGCTCTATCTGGAATAATTTCTCGGAATTCCT 477
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1995 CAATCGCAGGAGAACTCGGACACATCACCAAGCTGAAGCCCTGGAGCTCTTTGATGT 2054
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

476	DB	CAATCGCAGAGGAGAACTCGCACACATCCACCAAGCTGAAGCCCTGGAGCCTCTTTGATGT	417
2055	QY	ACTTGTGGAAAAGTATGGCTGGCCCCCATGAAGATGCTGCACAGTTTACAGATTTCTCTGAT	2114
416	DB	ACTTGTGGAAAAGTATGGCTGGCCCATGAAGATGCTGCACAGTTTACAGATTTCTCTGAT	357
2115	QY	CCGATGTTTGAANAATGGTTCAGNAAAAACAGAGCTCAGCTGGCGAATGCCCTTCGGCATCC	2174
356	DB	CCGATGTTTGAANAATGGTTCAGNAAAAACAGAGCTCAGCTGGCGAATGCCCTTCGGCATCC	297
2175	QY	TTGGTTCGAATTCCTTAGCAAAATTCACCAATATTGCAATCTTGAGCTAGCAAAATGTTCCCGAG	2234
296	DB	TTGGTTCGAATTCCTTAGCAAAATTCACCAATATTGCAATCTTGAGCTAGCAAAATGTTCCCGAG	237
2235	QY	TACATTTGGACCTAAACCGGTGACTCTCATTTCTTTAAACAGGAATTAACAGTAGCTGGCTTCA	2294
236	DB	TACATTTGGACCTAAACCGGTGACTCTCATTTCTTTAAACAGGAATTAACAGTAGCTGGCTTCA	177
2295	QY	TCCTCAGACCTTTAATTTTGGCTTTGAGGTACTGTTGTTTGACATTTTGGCTTTTGTGCGACT	2354
176	DB	TCCTCAGACCTTTAATTTTGGCTTTGAGGTACTGTTGTTTGACATTTTGGCTTTTGTGCGACT	117
2355	QY	GTGATCTCTGGGAAGGGTAGTCTTTTGTCTTCAGCTAAGTAGTTTACTGACCATTTTTCTT	2414
116	DB	GTGATCTCTGGGAAGGGTAGTCTTTTGTCTTCAGCTAAGTAGTTTACTGACCATTTTTCTT	57
2415	QY	CTGGAAAACAATAACATGCTCTTAAGCAATTG	2444
56	DB	CTGGAAAACAATAACATGCTCTTAAGCAATTG	27

RESULT	10
BUI6874	
LOCUS	
DEFINITION	BUI6874. 867 bp mRNA linear EST 04-SEP-2002 AGENCOURT_7960371 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166382 5', mRNA sequence.

Accession number: BUI166874.1 GI: 22680826
 Version: BUI166874.1
 Keywords: EST.
 Source: Homo sapiens (human)
 Organism: Homo sapiens
 Eukaryota; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 867)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Journal:
 Contact: Robert Strausberg, Ph.D.
 Comment:

FEATURES
source

ORIGIN

Query Match	24.1%	Score 785	DB 5	Length 867
Best Local Similarity	96.1%	Pred. No. 6.1e-166		
Matches 827	Conservative	0	Mismatches 30	Indels 4
Gaps	2			
QY	1210	GAAGATGATGTAGATCAGGAACCTTGGCAACATAGACCCCTACGTGGATAGAAATCACCTAAA	1269	
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QY	1270	ACCAATGGCCATATTGAGAAATGGCCCAATCTCTACTGGAGCAGCAACTGGACGATGAAGAT	1329	
DB	61	ACCAATGGCCATATTGAGAAATGGCCCAATCTCTACTGGAGCAGCAACTGGACGATGAAGAT	120	
QY	1330	GATGATGAAGAAGACATGCCCAAACTCTGAGGAATAATACTCTGATGAGCCAAATGCAGAA	1389	
DB	121	GATGATGAAGAAGACATGCCCAAACTCTGAGGAATAATACTCTGATGAGCCAAATGCAGAA	180	
QY	1390	AGTGATTACATATATAGCAGCTCCTATGAACAAATCAATGGTGAATGGCCAAATGCACGA	1449	
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QY	1510	GAACCTGTGCCCTGCGGCTCTGTGCTTTCTGAGGGATCACCACTTACTGACGAAGGAG	1569	
DB	301	GAACCTGTGCCCTGCGGCTCTGTGCTTTCTGAGGGATCACCACTTACTGACGAAGGAG	360	
QY	1570	AGCAGTCCATCCCATGACAGAACAGAA CGGTTTTCAGCCTTCAGTACTGGGATTTGCCA	1629	
DB	361	AGCAGTCCATCCCATGACAGAACAGGTTTTCAGCCTTCAGTACTGGGATTTGCCA	420	
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DB	541	GAAGACATCCAGACCGGTGAGTACCGCTCCATAGAGGTTTTTAATAGAGCGGGGTACAGC	600	
QY	1810	ACCCCTCGGACATCTGGAGCACGGGTGTATGGCAATTTGAGCTGGCAACCGGAGATTAT	1869	
DB	601	ACCCCTCGGACATCTGGAGCACGGGTGTATGGCAATTTGAGCTGGCAACCGGAGATTAT	660	
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QY	1930	ATAGAGCTGTAGGACGATTTCCAAGGCATTTGCTCTATCTGGAATAATTTCTCGGGAA	1989	
DB	721	ATAGAGCTGTAGGACGATTTCCAAGGCATTTGCTCTATCTGGAATAATTTCTCGGGAA	780	
QY	1990	TTCTTCAATCCGAGA -GGAGAACTGGACACATCACCAA - -GCTGAAGCCCTGGAGCCT	2045	
DB	781	TTCTTCAATCCGAGAAGGAAAAATGACCCCATCACCCAAAGCTGGAAAGCCCGGAACCCC	840	
QY	2046	CTTTGATGCTACTTGTGAAAA 2066		
DB	841	CTTTGATGCTACTTGTGAAAA 861		
RESULT 11				
LOCUS	BU182305	860 bp	mRNA	linear
DEFINITION	AGENCOURT_7840400 NIH_MGC_67 Homo sapiens			cdna clone IMAGE:6146259
ACCESSION	BU182305			
VERSION	BU182305.1			
KEYWORDS	EST.			

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 860)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13474 row: d column: 04
High quality sequence stop: 676.
FEATURES
Location/Qualifiers
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/tissue_type="retinoblastoma"
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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
Technologies."
ORIGIN
Query Match 23.5%; Score 765.2; DB 5; Length 860;
Best Local Similarity 97.9%; Pred. No. 1.8e-161;
Matches 797; Conservative 0; Mismatches 13; Indels 4; Gaps 2;
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QY 1988 AATTTCTCAATCGCAGAGAGAGTGCACACATCACCAGCTGAAGCCCTCGAGCCTCT 2047
DB 61 AATTTCTCAATCGCAGAGAGAGTGCACACATCACCAGCTGAAGCCCTCGAGCCTCT 120
QY 2048 TTGATGTACTTGTGGAAGAGTATGGCTGCGCCCATGAAGATGCTGCACAGTTTACAGATT 2107
DB 121 TTGATGTACTTGTGGAAGAGTATGGCTGCGCCCATGAAGATGCTGCACAGTTTACAGATT 180
QY 2108 TCTGATCCGATGTTAGAAATGGTTTCAGAAACAGACCTCAGTGGCGAATGCTTTC 2167
DB 181 TCTGATCCGATGTTAGAAATGGTTTCAGAAACAGACCTCAGTGGCGAATGCTTTC 240
QY 2168 GGCATCTTGGTGTGAATCTTAGCAATTTCTACCAATATTGATCTGAGCTAGCAAAATG 2227
DB 241 GGCATCTTGGTGTGAATCTTAGCAATTTCTACCAATATTGATCTGAGCTAGCAAAATG 300
QY 2228 TTCCAGTACATTTGACACCTTAAACGGTGAATCTCATTTCTTTAACAGGATTTACAGTGAGCT 2287
DB 301 TTCCAGTACATTTGACACCTTAAACGGTGAATCTCATTTCTTTAACAGGATTTACAGTGAGCT 360
QY 2288 GGCCTCATCTCAGACCTTTATTTGCTTTGAGGACTGTTGTTGACATTTTGTCTTTT 2347
DB 361 GGCCTCATCTCAGACCTTTATTTGCTTTGAGGACTGTTGTTGACATTTTGTCTTTT 420
QY 2348 GTGCACTGTGATCCGGGAGAGGTAGTCTTTTGTCTTCCAGCTAGTACTGATTTACTGACCA 2407
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QY 2408 TTTTCTTCTGGAACCAATACATGCTCTAAGCATTTGTTTCTTGTGTTGTGATTCATTC 2467
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QY 2528 ATTTATGAAGAAATATTTTAGCTGAGTACTATATAATTTTACAATCTTAAGAAATTTATCAA 2587
DB 601 ATTTATGAAGAAATATTTTAGCTGAGTACTATATAATTTTACAATCTTAAGAAATTTATCAA 660
QY 2588 GTTGGAAACCAAGAAATAGCAAGGAATGTACAATTTTATCTTCTGCAAGGACAT 2647
DB 661 GTTGGAAACCAAGAAATA---GCAAGGAATGTACAATTTTATCTTCTGCAAGGACAT 717
QY 2648 CATTCTCTATTTATGCTGATGTAATGCAACCTGTAATGTTACTTTCGATTAATATG 2707
DB 718 CATTCTCTATTTATGCTGATGTAATGCAACCTGTAATGTTACTTTCGATTAATATG 777
QY 2708 GGAGGGGGGACTCAAAATTTTCAGAAAGCTTAAAAA 2741
DB 778 GGA-GGGGGACTCAAAATTTTCAGAAAGCTTACCAA 810
RESULT 12
AUI24932
LOCUS AUI24932 NT2RM4 Homo sapiens cDNA clone NT2RM4000760 5', mRNA
DEFINITION AUI24932 828 bp mRNA linear EST 01-AUG-2002
ACCESSION AUI24932
VERSION AUI24932.1 GI:10949648
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 828)
AUTHORS Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J.,
Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and
Isogai, T.
TITLE HRI human cDNA project (Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S.,
Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T.,
Suzuki, Y., Sugano, S., Isogai, T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takeo Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM4000760"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RM4"
/note="Vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
ORIGIN
Query Match 23.3%; Score 759.2; DB 1; Length 828;
Best Local Similarity 98.8%; Pred. No. 4e-160;
Matches 795; Conservative 0; Mismatches 6; Indels 4; Gaps 3;
QY 1337 AAGAAGACTGCCCAATCTGAGGAAATATAATTTGATGAGGCAAAATGCAAAAGTGATT 1396
DB 14 AAGAAGACTGCCCAATCTGAGGAAATATAATTTGATGAGGCAAAATGCAAAAGTGATT 73

Db 601 GACGACATAAATCCCGAGTCACAGTCCCGCAGAGTTTCCACCTCGTGTCTCTGGA 660
Qy 1504 TCCTTAGAACCTGTGGCTCGCGCTCTGTGCTTTCTGAGGGATCACCATTACTGAGCAA 1563
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Qy 1564 GA-GGAGAGCAGTCCATCCATGACAGAGCAGAC-GGTTTCAGCCTCCAG--TACTGG 1619
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Db 781 GGATTTGCCAAAAGCAAAACCCCGGCGAGCTGACCGGTTTGTGGAATCCCTGGATC 840
Qy 1676 CCG-GGAATGAGATAAAA-TTAGAGTAAAAATG-CTGACCTGGGAAA---TGCTTGT 1729
Db 841 CCGGGAAGCAGATAAAATTTAGAGTAAAAATTCCTGACCTGAGAAAATGCCTTGGTG 900
Qy 1730 GGGTGCATAAACACTTCAGGAA 1752
Db 901 GGGGCGATAAACCTTTCGGAA 923

RESULT 14
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LOCUS BX423898 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
DEFINITION CSODN003YA14 5-PRIME, mRNA sequence.
ACCESSION BX423898
VERSION BX423898.2 GI:46927093
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 900)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 13, 2003 this sequence version replaced gi:30643492.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 4027.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSIAN0012E08QP1&c=4027.r.
Location/Qualifiers
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/clone="CSODN003YA14"
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/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

FEATURES

source
1..900
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODN003YA14"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match 22.8%; Score 741.8; DB 5; Length 900;
Best Local Similarity 97.0%; Pred. No. 3,5e-156;
Matches 808; Conservative 2; Mismatches 14; Indels 9; Gaps 5;

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Qy 970 TTGGAGAAGC--GCCTGCAGGAGATAGAGAAATTGGAGCGAAGAGCTGAAAGAAAATAA 1027
Db 65 TTGGAGAAGCAGCGCTCGCAGGAGATAGAGAAATTGGAGCGAAGAGCTGAAAGAAAATAA 124
Qy 1028 TAGAAGAAAAATCACTCTCAGCTGACCTTCCAAATGACAGATGCGGATGCTGCCAG 1087
Db 125 TAGAAGAAAAATCACTCTCAGCTGACCTTCCAAATGACAGATGCGGATGCTGCCAG 184
Qy 1088 AGGTCAACTTAAATAACAACAGGATTAGAGAGCGGCTGAGGACAGAGCTGCAAAAGACA 1147
Db 185 AGGTCAACTTAAATAACAACAGGATTAGAGAGCGGCTGAGGACAGAGCTGCAAAAGACA 244
Qy 1148 ATGGTGAAGCTGAGGACCGAGAGAGAGAGATGCTGAGAAAGAAAACATTGAAAAAG 1207
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Qy 1268 AAACCAATGGCCATATTGAGATGCGCCATTTCTCACTGGAGCAGCAACTGGACGATGAAG 1327
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Db 725 CAAAAGCAAAACCCGGGCGAGCTGACCTGTTGTTGTAATCCCTCGATCCGCGG-ATGCA 782
Qy 1687 GATAAAATTAGAGTAAATAATTCCTGACCTGGGAAATGCTTGTGGTGATAA 1739
Db 783 GATAAAATTAGAGTAAATAATTSIG---ACTKGGGAATGCTTGTGGTGATAA 831

RESULT 15

LOCUS BX442846
DEFINITION BX442846 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
ACCESSION BX442846
VERSION BX442846.2 GI:47037734
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 960)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)

QY 181 GCTCCTTTAGTTCCTCTCTCCACCGCCACCAACCAACCCACCTTTGCGAGAC 240
Db 181 GCTCCTTTAGTTCCTCTCTCCACCGCCACCAACCAACCCACCTTTGCGAGAC 240
QY 241 CCCACACCCCGGAGCAGAGAGAGATCTGGGATCAGATGATGAGGAGCAAGAGAC 300
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QY 301 CCGTGGGACTACTGCAAGAGTGATATCATCCAGTGAATAATGGAGACCTCTTCAATGGC 360
Db 301 CCGTGGGACTACTGCAAGAGTGATATCATCCAGTGAATAATGGAGACCTCTTCAATGGC 360
QY 361 CGGTATCATGTTATTAGAAAGCTTGATGGGGCACTTCTCTPACTGTCTGGCTGTGCTGG 420
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Db 421 GATATGCGAGGGAAGATTTGTTGCAATGAAGTGTGAAGAGTCCCGAGCATTTATAG 480
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Db 481 GAGACAGCTTCGATGAATAAAATTTGCTCAAAATGTTGCGAGAAAGTGATCCCAAGTGAC 540
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QY 841 CAGAAAGCAGGTGCTCCTCTCTCAGGCTCTGAGTACGGCTCCAAGCAGAAA 900
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QY 901 CCTATAGGAAAATATCTTAAAAACAAAAGAAAACCTGAAAAGAAAAGAGG 960
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QY 1261 TCACCTAAAACCAATGGCCATATTGAGAAATGGCCATTTCTCACTGGAGCAGCAACTGAC 1320
Db 1261 TCACCTAAAACCAATGGCCATATTGAGAAATGGCCATTTCTCACTGGAGCAGCAACTGAC 1320
QY 1321 GATGAAGATGATGATGAAGAGACTGCCAAATCTGAGGAATATAATCTTTGATGAGCA 1380
Db 1321 GATGAAGATGATGATGAAGAGACTGCCAAATCTGAGGAATATAATCTTTGATGAGCA 1380
QY 1381 AATGAGAAAGTATTACATATAGCAGCTCTTATGAACAAATTCATTTGATGAAATGGCA 1440
Db 1381 AATGAGAAAGTATTACATATAGCAGCTCTTATGAACAAATTCATTTGATGAAATGGCA 1440
QY 1441 AATGAGCAGATAAAATTTCCCGAGTCCAGTTCAGAGTTCCTGCTGCTCT 1500
Db 1441 AATGAGCAGATAAAATTTCCCGAGTCCAGTTCAGAGTTCCTGCTGCTCT 1500
QY 1501 GGATCTTTAGAACCTGTGGCTCTGCTCTCTGAGGATCACCACTTACTGAG 1560
Db 1501 GGATCTTTAGAACCTGTGGCTCTGCTCTCTGAGGATCACCACTTACTGAG 1560
QY 1561 CAAGAGGAGAGCAGTCCATCCATGACAGAAAGCAGACGGTTTCAGCTTACTGG 1620
Db 1561 CAAGAGGAGAGCAGTCCATCCATGACAGAAAGCAGACGGTTTCAGCTTACTGG 1620
QY 1621 GATTTGCCAAAAGCAAAACCCGGCAGTCTGCTGCTGAGGATCCCTGATCCGCG 1680
Db 1621 GATTTGCCAAAAGCAAAACCCGGCAGTCTGCTGCTGAGGATCCCTGATCCGCG 1680
QY 1681 AATGAGATAAAATTTAGAGTAAAAATCTGACCTGGGAAATGCTTTGGTGCATAAA 1740
Db 1681 AATGAGATAAAATTTAGAGTAAAAATTTGCTGACCTGGGAAATGCTTTGGTGCATAAA 1740
QY 1741 CACTTCCGGAAGACATCCAGACCGCTCAGTACCGCTCCATAGAGTTTAAATAGGAGC 1800
Db 1741 CACTTCCGGAAGACATCCAGACCGCTCAGTACCGCTCCATAGAGTTTAAATAGGAGC 1800
QY 1801 GGGTACAGACCCCTGGGACATCTGGAGCAGCGGTGATGGCATTTGAGCTGGCAACG 1860
Db 1801 GGGTACAGACCCCTGGGACATCTGGAGCAGCGGTGATGGCATTTGAGCTGGCAACG 1860
QY 1861 GGAGATTTATTTGTTGAACCACTTCTGGGGAAGACTATTCCAGAGACGAAGACACATA 1920
Db 1861 GGAGATTTATTTGTTGAACCACTTCTGGGGAAGACTATTCCAGAGACGAAGACACATA 1920
QY 1921 GCCACATCATAGAGCTGCTAGGCAAGTATTCAAAGGCACTTTGCTCTATCTGGAATAAT 1980
Db 1921 GCCACATCATAGAGCTGCTAGGCAAGTATTCAAAGGCACTTTGCTCTATCTGGAATAAT 1980
QY 1981 TCTCGGGAATTTCTCAATCGCAGAGGAGAACTGCGACACATCCCAAGCTGAAGCCCTGG 2040
Db 1981 TCTCGGGAATTTCTCAATCGCAGAGGAGAACTGCGACACATCCCAAGCTGAAGCCCTGG 2040
QY 2041 AGCTCTTTGATGTACTTTGTGAAAAGTATGGCTGGCCCATGAAGATGCTGCAAGTTT 2100
Db 2041 AGCTCTTTGATGTACTTTGTGAAAAGTATGGCTGGCCCATGAAGATGCTGCAAGTTT 2100
QY 2101 ACAGATTTCTGATCCCGATGTTAGAAATGGTTCCAGAAAAACGAGCCTCAGCTGGGAA 2160
Db 2101 ACAGATTTCTGATCCCGATGTTAGAAATGGTTCCAGAAAAACGAGCCTCAGCTGGGAA 2160
QY 2161 TGCCTTCGGCATCCTTGGTTGAAATTTAGCAAAATTTTACCAATATTCATTTCTGAGCTA 2220
Db 2161 TGCCTTCGGCATCCTTGGTTGAAATTTAGCAAAATTTTACCAATATTCATTTCTGAGCTA 2220
QY 2221 GCAATGTTCCAGTACATTTGACCTAAACCGTGACTCTCACTTTTAAACAGGATTACAA 2280
Db 2221 GCAATGTTCCAGTACATTTGACCTAAACCGTGACTCTCACTTTTAAACAGGATTACAA 2280
QY 2281 GTGAGCTGGCTTCACTCAGACCTTTATTTTGTCTTGGAGTACTGTTTGTGACATTTT 2340
Db 2281 GTGAGCTGGCTTCACTCAGACCTTTATTTTGTCTTGGAGTACTGTTTGTGACATTTT 2340
QY 2341 GCTTTTGTGCACTGCTGATCTCGGGAAGGGTAGTCTTTTGTCTTCAAGTAGTAGTTA 2400

Db 2341 GCCTTTTGTGCACTGTGATCTCTGGGAGGGTAGTCTTTTGTCTTCAGCTAGTAGTTTA 2400
QY 2401 CTGACCAATTTCTCTTGGAAACAATAACATGCTCTTAAGCATTTCTTGTGTTGTG 2460
Db 2401 CTGACCAATTTCTCTTGGAAACAATAACATGCTCTTAAGCATTTCTTGTGTTGTG 2460
QY 2461 ACATTCAAAATGTCATTTTCTTGAATGAAAATACTTTCCCTTTGTGTTTGGCAGGTTT 2520
Db 2461 ACATTCAAAATGTCATTTTCTTGAATGAAAATACTTTCCCTTTGTGTTTGGCAGGTTT 2520
QY 2521 TGTAACTATTATGAAGAAATATTTTAGCTGAGTACTATATATATTTTACAACTCTTAAGAAA 2580
Db 2521 TGTAACTATTATGAAGAAATATTTTAGCTGAGTACTATATATATTTTACAACTCTTAAGAAA 2580
QY 2581 TTATCAAGTTGGAAACCAAGAAATAGCAAGGAAATGTACAAATTTTATCTTCTGCAAA 2640
Db 2581 TTATCAAGTTGGAAACCAAGAAATAGCAAGGAAATGTACAAATTTTATCTTCTGCAAA 2640
QY 2641 GGGACATCATTTCTGTATTATAGTGTATGTAAATGCAACCTGTAAATGTACTTTGGATT 2700
Db 2641 GGGACATCATTTCTGTATTATAGTGTATGTAAATGCAACCTGTAAATGTACTTTGGATT 2700
QY 2701 AAATATGCGAGGGGGACTCAAAATTTTCAAGAAAGCTTAAAAAAGGTAATAAGG 2760
Db 2701 AAATATGCGAGGGGGACTCAAAATTTTCAAGAAAGCTTAAAAAAGGTAATAAGG 2760
QY 2761 AAAAATACCTTATATTAATAATACCTTTCTTTTGTGTTTCTTATTTTCAATTT 2820
Db 2761 AAAAATACCTTATATTAATAATACCTTTCTTTTGTGTTTCTTATTTTCAATTT 2820
QY 2821 ATTAATACACTTAACCTTTGCGAAAGCACTATGAAAAAATTAATACCATGAAAGATCA 2880
Db 2821 ATTAATACACTTAACCTTTGCGAAAGCACTATGAAAAAATTAATACCATGAAAGATCA 2880
QY 2881 AAAATCATAAATCAAAACCCACTATAGTCCAAAGCAATTCATTTCTGCGCGTCAACTT 2940
Db 2881 AAAATCATAAATCAAAACCCACTATAGTCCAAAGCAATTCATTTCTGCGCGTCAACTT 2940
QY 2941 TTTAATCATCTTATAGTACCTGAGACTCTGCTGCTCAATATTAATTTCTAAATCTAC 3000
Db 2941 TTTAATCATCTTATAGTACCTGAGACTCTGCTGCTCAATATTAATTTCTAAATCTAC 3000
QY 3001 CACCAAGTTAGGCCCCGTAATGCTCTCTCTGCTGAACTGTGTCATACATATTTTCT 3060
Db 3001 CACCAAGTTAGGCCCCGTAATGCTCTCTCTGCTGAACTGTGTCATACATATTTTCT 3060
QY 3061 ATTTATTTAGTGGCTCTCGTTTATCTTTTCGCCACATCTTTGTTCACTATTTCTAGTTA 3120
Db 3061 ATTTATTTAGTGGCTCTCGTTTATCTTTTCGCCACATCTTTGTTCACTATTTCTAGTTA 3120
QY 3121 CTCTTATCTTTGGGCTGATTAATCTTCTCATTTATCTCATATAAATCTTCTGAATTTTTC 3180
Db 3121 CTCTTATCTTTGGGCTGATTAATCTTCTCATTTATCTCATATAAATCTTCTGAATTTTTC 3180
QY 3181 ACATAAACTACTAGAGTACCTCACAATCTCTGTTTTTAAACGAGAGGATTAATATA 3240
Db 3181 ACATAAACTACTAGAGTACCTCACAATCTCTGTTTTTAAACGAGAGGATTAATATA 3240
QY 3241 ATTACTATTAAA 3253
Db 3241 ATTACTATTAAA 3253

RESULT 2
US-10-207-973-1
; Sequence 1, Application US/10207973
; Publication No. US20030175927A1
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/10/207,973
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3253
; TYPE: DNA
; ORGANISM: Human
; US-10-207-973-1

Query Match 100.0%; Score 3253; DB 15; Length 3253;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCGGAGCGAGTGGAGGCTGCAGCCAGCTCGTCTCGGCGCCCGCGTGGCGTGGCGG 60
Db 1 TCGCGGAGCGAGTGGAGGCTGCAGCCAGCTCGTCTCGGCGCCCGCGTGGCGTGGCGG 60
QY 61 AGCCCCCGCCCGCTTCGCGCGCTCGGAATGAGTCCCGGAAAGTCTGGCCATTGAG 120
Db 61 AGCCCCCGCCCGCTTCGCGCGCTCGGAATGAGTCCCGGAAAGTCTGGCCATTGAG 120
QY 121 GCCCGAAAGCGAGGCGGAAAGAGAGAAACATCCGAAAAAGCCGAGGCTCAACAGAAA 180
Db 121 GCCCGAAAGCGAGGCGGAAAGAGAGAAACATCCGAAAAAGCCGAGGCTCAACAGAAA 180
QY 181 GCTCCTTTAGTTTCTCTCTCCAGCCACCAACCACCCAGCCCTTTTGGCAGAC 240
Db 181 GCTCCTTTAGTTTCTCTCTCCAGCCACCAACCACCCAGCCCTTTTGGCAGAC 240
QY 241 CCCACACCCCGGAGGAGGAGGAGATCTTGGGATCAGATGATGAGGAGCAGAGGAC 300
Db 241 CCCACACCCCGGAGGAGGAGGAGATCTTGGGATCAGATGATGAGGAGCAGAGGAC 300
QY 301 CTTGGGAGCTACTGCAAAAGGTGATATCATCCAGTGAAATTTGGAGACCTCTTCAATGGC 360
Db 301 CTTGGGAGCTACTGCAAAAGGTGATATCATCCAGTGAAATTTGGAGACCTCTTCAATGGC 360
QY 361 CGGTATCATGTTATTAGAAAGCTTGGATGGGGGCACTTCTCTACTGTCTGGCTGTCTGG 420
Db 361 CGGTATCATGTTATTAGAAAGCTTGGATGGGGGCACTTCTCTACTGTCTGGCTGTCTGG 420
QY 421 GATATGAGGGGAAAGATTTGTTGCAATGAAAGTTGTAAGTCCCGCAGCATTTATACG 480
Db 421 GATATGAGGGGAAAGATTTGTTGCAATGAAAGTTGTAAGTCCCGCAGCATTTATACG 480
QY 481 GAGACAGCCTTCGATGAAATAAAATTTGCTCAAAATGTTTCGAGAAAGTATCCAGTGAC 540
Db 481 GAGACAGCCTTCGATGAAATAAAATTTGCTCAAAATGTTTCGAGAAAGTATCCAGTGAC 540
QY 541 CCAAAACAAAGACATGGTGGTCCAGCTCATTTGACGACTTCAAGATTTTCAAGATTTGGG 600
Db 541 CCAAAACAAAGACATGGTGGTCCAGCTCATTTGACGACTTCAAGATTTTCAAGATTTGGG 600
QY 601 ATACATGTCTGATGTTGTTGAAAGTACTTGGCCACCATCTCTCAAGTGGATCATCAA 660
Db 601 ATACATGTCTGATGTTGTTGAAAGTACTTGGCCACCATCTCTCAAGTGGATCATCAA 660
QY 661 TCCAACTATCAAGGCTCCCGAGTACGTTGTTGTAAGAGTATCATTTCCAGAGGTCCTTCAA 720
Db 661 TCCAACTATCAAGGCTCCCGAGTACGTTGTTGTAAGAGTATCATTTCCAGAGGTCCTTCAA 720
QY 721 GGGTTAGATTACTTACACAGTAAGTCAAGATCATTTTCACTACTGACATAAGCCGGAAT 780
Db 721 GGGTTAGATTACTTACACAGTAAGTCAAGATCATTTTCACTACTGACATAAGCCGGAAT 780
QY 781 ATCTTGAATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
Db 781 ATCTTGAATGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 CAGAAAGCAGGTCCT 900
Db 841 CAGAAAGCAGGTCCT 900

D	b	841	CAGAAACGAGCTCCTCTCTCCCTTCAGGGTCTCGAGTGATACGGCTCCACAGCAAAA	900
Q	y	901	CCTATAGGAAAAATATCTAATAAACAAAAAGAAAACTGAAAAAGAAAAACAAGAGGCAG	960
D	b	901	CCTATAGGAAAAATATCTAATAAACAAAAAGAAAACTGAAAAAGAAAAACAAGAGGCAG	960
Q	y	961	GCTGACTTATTGGAGAAGCGCTCGAGAGATAGAGAATTTGGAGCGAGAAGCTGAAGG	1020
D	b	961	GCTGACTTATTGGAGAAGCGCTCGAGAGATAGAGAATTTGGAGCGAGAAGCTGAAGG	1020
Q	y	1021	AAATTAATAGAAAGAAACATCACCTCAGCTCAGCTCCATTCACAGGATGGCGAATAC	1080
D	b	1021	AAATTAATAGAAAGAAACATCACCTCAGCTCAGCTCCATTCACAGGATGGCGAATAC	1080
Q	y	1081	TGCCCAGAGGTGAAACTAATAAAACAACAGGATTTAGAGGAGCGGTGAGGAGAGATGCA	1140
D	b	1081	TGCCCAGAGGTGAAACTAATAAAACAACAGGATTTAGAGGAGCGGTGAGGAGAGATGCA	1140
Q	y	1141	AAGGACAAATGGTGAAGCTGAGGACAGGAAAGAAAGAAAGTCTGAGAAAGAAACATT	1200
D	b	1141	AAGGACAAATGGTGAAGCTGAGGACAGGAAAGAAAGAAAGTCTGAGAAAGAAACATT	1200
Q	y	1201	GAAAAAGATGAAGATGATGTAGATCAGGAATTTGCGAAACATAGACCCTTACGTGGATAGAA	1260
D	b	1201	GAAAAAGATGAAGATGATGTAGATCAGGAATTTGCGAAACATAGACCCTTACGTGGATAGAA	1260
Q	y	1261	TCACCTAAAAACCAATGGCCATTTAGAAATGGCCCCATTTCTCACTGGAGCAGCACTGGAC	1320
D	b	1261	TCACCTAAAAACCAATGGCCATTTAGAAATGGCCCCATTTCTCACTGGAGCAGCACTGGAC	1320
Q	y	1321	GATGAAGATCATGATGAAGAAGACTGCCCAAATCTCGAGGAATAAATCTTTGATGAGCCA	1380
D	b	1321	GATGAAGATCATGATGAAGAAGACTGCCCAAATCTCGAGGAATAAATCTTTGATGAGCCA	1380
Q	y	1381	AATGCAAGAAAGTGAATTACATATAGACAGCTCCTATGAACAAATTCATTTGATTTGCCA	1440
D	b	1381	AATGCAAGAAAGTGAATTACATATAGACAGCTCCTATGAACAAATTCATTTGATTTGCCA	1440
Q	y	1441	AATGGAGCAGATAAAATTTCCCGAGTCCACAGTTCACAGAGTTTTCCACCTCGTTGTTCTCT	1500
D	b	1441	AATGGAGCAGATAAAATTTCCCGAGTCCACAGTTCACAGAGTTTTCCACCTCGTTGTTCTCT	1500
Q	y	1501	GGATCCTTAGAAGCTGFGGCTCGGCTCTGTGCTTTCTGAGGATACCACTACTGAG	1560
D	b	1501	GGATCCTTAGAAGCTGFGGCTCGGCTCTGTGCTTTCTGAGGAGTACCACTACTGAG	1560
Q	y	1561	CAAGAGGAGCAGTCCATCCCATGACAGAGCAGAAACGGTTTCAGCCCTCCAGTACTGGG	1620
D	b	1561	CAAGAGGAGCAGTCCATCCCATGACAGAGCAGAAACGGTTTCAGCCCTCCAGTACTGGG	1620
Q	y	1621	GATTTGCCAAAAGCAAAAACCCGGGAGCTGACTTTCTGGTGAATCCCTCGATCCGGGG	1680
D	b	1621	GATTTGCCAAAAGCAAAAACCCGGGAGCTGACTTTCTGGTGAATCCCTCGATCCGGGG	1680
Q	y	1681	AATGAGATTAATTTAGAGTAAATTTGCTGACCTGGGAATGCTTTGTTGGTGCATAAA	1740
D	b	1681	AATGAGATTAATTTAGAGTAAATTTGCTGACCTGGGAATGCTTTGTTGGTGCATAAA	1740
Q	y	1741	CACTTTCAGGAAGACATCCAGACCGTFCAGTACCGCTCCATAGAGTTTTAATAGAGCG	1800
D	b	1741	CACTTTCAGGAAGACATCCAGACCGTFCAGTACCGCTCCATAGAGTTTTAATAGAGCG	1800
Q	y	1801	GGGTHACAGACCCCTGGGACATCTGAGACCGGCTGTATGCAATTCAGCTGGCAACG	1860
D	b	1801	GGGTHACAGACCCCTGGGACATCTGAGACCGGCTGTATGCAATTCAGCTGGCAACG	1860
Q	y	1861	GGAGATTAATTTGTTGAACCAATCTTGGGGAAGACTAATTCAGAGACGAAGACACATA	1920
D	b	1861	GGAGATTAATTTGTTGAACCAATCTTGGGGAAGACTAATTCAGAGACGAAGACACATA	1920
Q	y	1921	GCCCAATCATAGAGCTGCTAGGAGATTTCCAAAGGCACTTTGCTCTATCTGGAANAAT	1980
D	b	1921	GCCCAATCATAGAGCTGCTAGGAGATTTCCAAAGGCACTTTGCTCTATCTGGAANAAT	1980

QY 3061 ATTATTAGTGGCTCGTTTATCTTTTCGCCACATCTTTGTTCACTATTTTCTAGTTA 3120
DB 3061 ATTATTAGTGGCTCGTTTATCTTTTCGCCACATCTTTGTTCACTATTTTCTAGTTA 3120
QY 3121 CTCCTATCTTTGGCTGATTAAATCTCTCTCATTTATCTCATATAAACTTCTGAATTTTC 3180
DB 3121 CTCCTATCTTTGGCTGATTAAATCTCTCTCATTTATCTCATATAAACTTCTGAATTTTC 3180
QY 3181 ACATAAACTACTAGAGCTACCTCACCATCTCTGTTTTTAAACCGAGGAGTTACTATATA 3240
DB 3181 ACATAAACTACTAGAGCTACCTCACCATCTCTGTTTTTAAACCGAGGAGTTACTATATA 3240
QY 3241 ATTACTATTAAA 3253
DB 3241 ATTACTATTAAA 3253

RESULT 3

US-10-799-676-1
; Sequence 1, Application US/10799676
; Publication No. US20040157297A1
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001043DIV II
; CURRENT APPLICATION NUMBER: US/10/799,676
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: 10/207,973
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 09/759,359
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3253
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-799-676-1

Query Match 100.0%; Score 3253; DB 17; Length 3253;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGCGGAGCGAGTGAGGCTGCAGCCAGCTCGTCTCGGCGCCCGCGTCGCCGTCGCGA 60
DB 1 TCGCGGAGCGAGTGAGGCTGCAGCCAGCTCGTCTCGGCGCCCGCGTCGCCGTCGCGA 60
QY 61 AGCCCCCGCCCGCTTCGCGCGCTCGGAATGAGCTCCGGAAGTGTGGCCATTTCAG 120
DB 61 AGCCCCCGCCCGCTTCGCGCGCTCGGAATGAGCTCCGGAAGTGTGGCCATTTCAG 120
QY 121 GCCCGAAGCGGAGCGGAGAAAGAGAAACATCCGAAAGCCGAGCCTCAACAGAAA 180
DB 121 GCCCGAAGCGGAGCGGAGAAAGAGAAACATCCGAAAGCCGAGCCTCAACAGAAA 180
QY 181 GCTCCTTTAGTTCTCTCTCCACCGCCACCAACACCCACCGCCTTTGGCAGAC 240
DB 181 GCTCCTTTAGTTCTCTCTCCACCGCCACCAACACCCACCGCCTTTGGCAGAC 240
QY 241 CCACACCCCGGAGCCAGAGGAGATCCTGGGATCAGATGAGAGCAAGGAGAC 300
DB 241 CCACACCCCGGAGCCAGAGGAGATCCTGGGATCAGATGAGAGCAAGGAGAC 300
QY 301 CTTGGGACTACTGCAAGGTTGATATCCAGTGAAATTTGGAGACCTCTCAATGGC 360
DB 301 CTTGGGACTACTGCAAGGTTGATATCCAGTGAAATTTGGAGACCTCTCAATGGC 360
QY 361 CGGTATCATGTTATTAGAAAGCTTGGATGGGGCACTTCTTACTGTCTGGCTGTGCTGG 420
DB 361 CGGTATCATGTTATTAGAAAGCTTGGATGGGGCACTTCTTACTGTCTGGCTGTGCTGG 420

QY 421 GATATGAGGGGAAAGATTTTGTCAATGAAAGTTGTAAAGTCCCCAGCATTATACG 480
DB 421 GATATGAGGGGAAAGATTTTGTCAATGAAAGTTGTAAAGTCCCCAGCATTATACG 480
QY 481 GAGACAGCCCTTGGATGAAATAAAATTTGCTCAAAATGTTTCGAGAAAGTATCCCACTGAC 540
DB 481 GAGACAGCCCTTGGATGAAATAAAATTTGCTCAAAATGTTTCGAGAAAGTATCCCACTGAC 540
QY 541 CCAAAACAAAGACATGGTGGTCCAGCTCATTTGACGACTTCAAGATTTTCAGGCATGAATGGG 600
DB 541 CCAAAACAAAGACATGGTGGTCCAGCTCATTTGACGACTTCAAGATTTTCAGGCATGAATGGG 600
QY 601 ATACATGCTGCTGATGCTCTTTCGAAAGTACTTGGCCACCCTCTCTCAAGTGGATCATCAA 660
DB 601 ATACATGCTGCTGATGCTCTTTCGAAAGTACTTGGCCACCCTCTCTCAAGTGGATCATCAA 660
QY 661 TCCAACTATCAAGGCTCTCCAGTACGTTGTGTGAAGAGTATCATTCGACAGGTCCTTCAA 720
DB 661 TCCAACTATCAAGGCTCTCCAGTACGTTGTGTGAAGAGTATCATTCGACAGGTCCTTCAA 720
QY 721 GGGTTAGATTACTTACACAGTAAAGTGCAGATCATTTATCTGACATATAAGCCGGAAT 780
DB 721 GGGTTAGATTACTTACACAGTAAAGTGCAGATCATTTATCTGACATATAAGCCGGAAT 780
QY 781 ATCTTTGATGCTGTGGATGATGCATATGTGAAGAAATGGCAGCTGAGGCCATGAGTGG 840
DB 781 ATCTTTGATGCTGTGGATGATGCATATGTGAAGAAATGGCAGCTGAGGCCATGAGTGG 840
QY 841 CAGAAAGCAGGTCCTCTCTCTCCTTTCAGGCTCTGAGTACGCTCCACAGCAGAAA 900
DB 841 CAGAAAGCAGGTCCTCTCTCTCCTTTCAGGCTCTGAGTACGCTCCACAGCAGAAA 900
QY 901 CCTATAGGAAAAATATCTAAAAACAAAAAGAAAACTGAAAAAGAAAAAGAGAGGAG 960
DB 901 CCTATAGGAAAAATATCTAAAAACAAAAAGAAAACTGAAAAAGAAAAAGAGAGGAG 960
QY 961 GCTGAGTTATTGGAGAGCGCTCGAGGAGATGAGAGATTTGGAGCGAGAACTGAAGG 1020
DB 961 GCTGAGTTATTGGAGAGCGCTCGAGGAGATGAGAGATTTGGAGCGAGAACTGAAGG 1020
QY 1021 AAAATAATAGAAAAAATACACCTCAGCTGCACCTTCCAAATGACAGAGTCCGCAATAC 1080
DB 1021 AAAATAATAGAAAAAATACACCTCAGCTGCACCTTCCAAATGACAGAGTCCGCAATAC 1080
QY 1081 TGCCCGAGGTTGAAACTAAAAACAACAGGATTAGAGGAGCGGCTGAGCAGAGACTGCA 1140
DB 1081 TGCCCGAGGTTGAAACTAAAAACAACAGGATTAGAGGAGCGGCTGAGCAGAGACTGCA 1140
QY 1141 AAGGCAATGTTGAAGCTGAGGACAGGAGAAAGAGATGCTGAGAGAAAGAAACATT 1200
DB 1141 AAGGCAATGTTGAAGCTGAGGACAGGAGAAAGAGATGCTGAGAGAAAGAAACATT 1200
QY 1201 GAAAAAGATGAAGATGATGATAGATCAGGAACTTTCGAAACATAGACCTACGTTGAGAA 1260
DB 1201 GAAAAAGATGAAGATGATGATAGATCAGGAACTTTCGAAACATAGACCTACGTTGAGAA 1260
QY 1261 TCACCTAAACCAATGGCCATATTGAGAAATGGCCCATTTCTCACTGGAGCAGCAACTGGAC 1320
DB 1261 TCACCTAAACCAATGGCCATATTGAGAAATGGCCCATTTCTCACTGGAGCAGCAACTGGAC 1320
QY 1321 GATGAAGATGATGATGAAGAGACTGCCCCAAATCTCTGAGGAATATATCTTGTATGAGCCA 1380
DB 1321 GATGAAGATGATGATGAAGAGACTGCCCCAAATCTCTGAGGAATATATCTTGTATGAGCCA 1380
QY 1381 AATGAGAAAGTATTACACATATAGCAGCTCCTTGAACAAATTCATGAAATTTGCAATTTGCCA 1440
DB 1381 AATGAGAAAGTATTACACATATAGCAGCTCCTTGAACAAATTCATGAAATTTGCAATTTGCCA 1440
QY 1441 AATGAGCAGCATATAAATTTCCCGAGTCACAGTTTCCAGAGTCTTCCACCTCGTTGTTCTCT 1500
DB 1441 AATGAGCAGCATATAAATTTCCCGAGTCACAGTTTCCAGAGTCTTCCACCTCGTTGTTCTCT 1500
QY 1501 GGATCCTTAGAAACCTGTGGCCTGTGGCTCTGTCTTTCTGAGGGATCACCACTTACTGAG 1560

1501 GATCTCTTAGAACCTGTGGCTGGGCTCTGTGCTTTCTGAGGATCACCCTTACTGAG 1560
1561 CAAGAGGAGAGCAGTCCATCCATGACAGAGCAGAACCGTTTCAGCCCTCAGTACTGGG 1620
1561 CAAGAGGAGAGCAGTCCATCCATGACAGAGCAGAACCGTTTCAGCCCTCAGTACTGGG 1620
1621 GATTTGCCAAGACAAACCCGGCAGCTGACTTTGTTGGTGAATCCCTCGATCCGCGG 1680
1621 GATTTGCCAAGACAAACCCGGCAGCTGACTTTGTTGGTGAATCCCTCGATCCGCGG 1680
1681 AATGACAGATAAATTTAGAGTAAATTTGCTGACCTGGGAAATGCTTGTGGTGCATAAA 1740
1681 AATGACAGATAAATTTAGAGTAAATTTGCTGACCTGGGAAATGCTTGTGGTGCATAAA 1740
1741 CACTTCAGGAAGACATCCAGACGGTCCAGTACCCCTCATAGAGGTTTTAATAGGAGCG 1800
1741 CACTTCAGGAAGACATCCAGACGGTCCAGTACCCCTCATAGAGGTTTTAATAGGAGCG 1800
1801 GGGTACAGCACCCTCGGACATCTGGAGCAGCGGTGTATGGCATTTGAGCTGGCAACG 1860
1801 GGGTACAGCACCCTCGGACATCTGGAGCAGCGGTGTATGGCATTTGAGCTGGCAACG 1860
1861 GGAGATTATTTGTTGTAACCAATCTGGGGAAGACTATTCAGAGACGAAGACACATA 1920
1861 GGAGATTATTTGTTGTAACCAATCTGGGGAAGACTATTCAGAGACGAAGACACATA 1920
1921 GCCCAGATCAGAGCTGTAGGAGTATCCAGGCACTTTGCTCTATCTGGAATAAT 1980
1921 GCCCAGATCAGAGCTGTAGGAGTATCCAGGCACTTTGCTCTATCTGGAATAAT 1980
1981 TCTCGGGAATTTCTCAATCGCAGAGAGAACTGGCAGACATCACCAGCTGAAGCCCTGG 2040
1981 TCTCGGGAATTTCTCAATCGCAGAGAGAACTGGCAGACATCACCAGCTGAAGCCCTGG 2040
2041 AGCCTCTTTGATGTAATCTTGGAAGAAAGTATGGTGGCCCATGAGATGCTGCACAGTTT 2100
2041 AGCCTCTTTGATGTAATCTTGGAAGAAAGTATGGTGGCCCATGAGATGCTGCACAGTTT 2100
2101 ACAGATTTCTGATCCGATGTTAGAAATGGTTCCAGAAAAACGAGCCCTCAGCTGGCAA 2160
2101 ACAGATTTCTGATCCGATGTTAGAAATGGTTCCAGAAAAACGAGCCCTCAGCTGGCAA 2160
2161 TGCCCTTCGGCATCCTTTGGTGAATCTTAGCAAAATCTACCAATATGCAATCTGAGCTA 2220
2161 TGCCCTTCGGCATCCTTTGGTGAATCTTAGCAAAATCTACCAATATGCAATCTGAGCTA 2220
2221 GCAAAATGTTCCAGTACATGGACCTTAAACGGTGAATCTCTCTTTTAAACAGGATTACAA 2280
2221 GCAAAATGTTCCAGTACATGGACCTTAAACGGTGAATCTCTCTTTTAAACAGGATTACAA 2280
2281 GTGAGCTGGCTTCATCTCAGACCTTTATTTTCTTTGAGGTACTGTTGTTGACATTTT 2340
2281 GTGAGCTGGCTTCATCTCAGACCTTTATTTTCTTTGAGGTACTGTTGTTGACATTTT 2340
2341 GCCTTTTGTGCACTGTGATCCTCGGGAAGGTTAGTCTTTGCTTCAGCTAAGTAGTTTA 2400
2341 GCCTTTTGTGCACTGTGATCCTCGGGAAGGTTAGTCTTTGCTTCAGCTAAGTAGTTTA 2400
2401 CTGACCAATTTCTTCGGAACAAATACATGCTCTTAAGCAATGTTTCTGTTGTTG 2460
2401 CTGACCAATTTCTTCGGAACAAATACATGCTCTTAAGCAATGTTTCTGTTGTTG 2460
2461 ACATTCAAATGTCATTTTGTGATGAAAAATCTTTCCCTTTGTTTGGCAGGTTT 2520
2461 ACATTCAAATGTCATTTTGTGATGAAAAATCTTTCCCTTTGTTTGGCAGGTTT 2520
2521 TGTAACCTATTATGAAGAAATATTTTAGCTGAGTATATATATTTTCAATCTTACAAA 2580
2521 TGTAACCTATTATGAAGAAATATTTTAGCTGAGTATATATATTTTCAATCTTACAAA 2580
2581 TTATCAAGTTGGGAACCAAGAAATAGCAAGGGAATGTACATTTTATCTCTGGCAAA 2640

2581 TTATCAAGTTGGGAACCAAGAAATAGCAAGGGAATGTACATTTTATCTTCTGCAAA 2640
2641 GGGACATCATCTCTGTATTATAGTATAATGCAACCTGTAAATGTTACTTTGGATT 2700
2641 GGGACATCATCTCTGTATTATAGTATAATGCAACCTGTAAATGTTACTTTGGATT 2700
2701 AAATATGGGAGGGGAGCTCAAAATTTTCAGAAAGCTTAAAAAAGTAAAGG 2760
2701 AAATATGGGAGGGGAGCTCAAAATTTTCAGAAAGCTTAAAAAAGTAAAGG 2760
2761 AAAAATCTCTTATATTAATACCTTCTTCTTTGTTTCTTATTTCTTATTTT 2820
2761 AAAAATCTCTTATATTAATACCTTCTTCTTTGTTTCTTATTTCTTATTTT 2820
2821 ATTAAATACACTTAAACGTTTCGAAAGCACTATGAAAGAAATTAATACATGAAAGGATCA 2880
2821 ATTAAATACACTTAAACGTTTCGAAAGCACTATGAAAGAAATTAATACATGAAAGGATCA 2880
2881 AAAATCATAAATCAAAACCCCACTATAGTCCAAACGCAATTCATTCGCGGGTCAACTT 2940
2881 AAAATCATAAATCAAAACCCCACTATAGTCCAAACGCAATTCATTCGCGGGTCAACTT 2940
2941 TTTAAACTCTTATATAGTACCTGAGACTCTGGTGTCTCAATATTAATTTCTAAATCTAC 3000
2941 TTTAAACTCTTATATAGTACCTGAGACTCTGGTGTCTCAATATTAATTTCTAAATCTAC 3000
3001 CACCAAGTTAGGCGCGTAATGTGCTCTCTCGTGAATCTGTCTATCAATACATTTTCT 3060
3001 CACCAAGTTAGGCGCGTAATGTGCTCTCTCGTGAATCTGTCTATCAATACATTTTCT 3060
3061 ATTTATTTAGTGGTCTCGTTTATCTTTCGCCACATCTTTGTTGTTCTAGTTA 3120
3061 ATTTATTTAGTGGTCTCGTTTATCTTTCGCCACATCTTTGTTGTTCTAGTTA 3120
3121 CTCTTATCTTTGGGCTGATTAATCTTCTCATATATCTCATATAAACTTCTGAATTTTC 3180
3121 CTCTTATCTTTGGGCTGATTAATCTTCTCATATATCTCATATAAACTTCTGAATTTTC 3180
3181 ACATAAACTACTAGAGCTACCTCACCATCTCTGTTTTTAAACGAGCAGTTACTATATA 3240
3181 ACATAAACTACTAGAGCTACCTCACCATCTCTGTTTTTAAACGAGCAGTTACTATATA 3240
3241 ATTACTATTTAAA 3253
3241 ATTACTATTTAAA 3253

RESULT 4

US-10-618-941-36
; Sequence 36, Application US/10618941
; Publication No. US20040197792A1
; GENERAL INFORMATION:
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: CAENEPEEL, SEAN
; TITLE OF INVENTION: NOVEL KINASES
; FILE REFERENCE: 034536-0321
; CURRENT APPLICATION NUMBER: US/10/618,941
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/395,632
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 3715
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-618-941-36

Query Match 77.9%; Score 2533.8; DB 18; Length 3715;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2568; Conservative 0; Mismatches 17; Indels 4; Gaps 2;

QY 153 TCCGAAAAAGCCGAGCCTCAACAGAAAGCTCCTTTAGTTCTCTCTCTCCACCGCCACC 212
DB 208 TTCAGAAAGCCGAGCCTCAACAGAAAGCTCCTTTAGTTCTCTCTCTCCACCGCCACC 267
QY 213 ACCACCAACACCGCCACCTTTTGCAGACGCCCAACACCCCGGAGCCAGAGAGAGATCCT 272
DB 268 ACCACCAACACCGCCACCTTTTGCAGACGCCCAACACCCCGGAGCCAGAGAGAGATCCT 327
QY 273 GGGATCAGATGATGAGGAGCAGAGGACCCCTCGGACTACTGCAAGGTGGATATCATCC 332
DB 328 GGGATCAGATGATGAGGAGCAGAGGACCCCTCGGACTACTGCAAGGTGGATATCATCC 387
QY 333 AGTGAATAATGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGGG 392
DB 388 AGTGAATAATGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGGG 447
QY 393 GCACCTTCTACTGTCTGTCTGTGGGATATGCAAGGGGAAAAGATTTGTTGCAATGAA 452
DB 448 GCACCTTCTACTGTCTGTCTGTGGGATATGCAAGGGGAAAAGATTTGTTGCAATGAA 507
QY 453 AGTTGTAATAAGTCCAGCATATATACGGAGACAGCCCTTGGATGAATAAATTTGCTCAA 512
DB 508 AGTTGTAATAAGTCCAGCATATATACGGAGACAGCCCTTGGATGAATAAATTTGCTCAA 567
QY 513 ATGTGTTTCGAGAAAGTGATCCCAAGTGACCCAAACAAAGACATGGTGGTCAATTCGA 572
DB 568 ATGTGTTTCGAGAAAGTGATCCCAAGTGACCCAAACAAAGACATGGTGGTCAATTCGA 627
QY 573 CGACCTTCAAGATTTTCAGGCATGAATGGGATACATGTCGTGATCTCCGAAAGTACTGG 632
DB 628 CGACCTTCAAGATTTTCAGGCATGAATGGGATACATGTCGTGATCTCCGAAAGTACTGG 687
QY 633 CCACCATCTCTCAAGTGATCATCAATCCAACTATCAAGGCCTCCAGAGTACTGGTGT 692
DB 688 CCACCATCTCTCAAGTGATCATCAATCCAACTATCAAGGCCTCCAGAGTACTGGTGT 747
QY 693 GAAGAGTATCATTTGAGACGCTCTTCAAGGGTTAGATTACTTACACAGTAAGTGAAGAT 752
DB 748 GAAGAGTATCATTTGAGACGCTCTTCAAGGGTTAGATTACTTACACAGTAAGTGAAGAT 807
QY 753 CATTTACTGACATAAAGCCCGAAAAATATCTTTGATGTGTGGATGATGCATATGTGAG 812
DB 808 CATTTACTGACATAAAGCCCGAAAAATATCTTTGATGTGTGGATGATGCATATGTGAG 867
QY 813 AAGAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGAGTGCTCTCTCTCTTCAGGGTC 872
DB 868 AAGAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGAGTGCTCTCTCTCTTCAGGGTC 927
QY 873 TGCAGTGAGTACGGCTCCACAGCAGAAACCTATAGGAAAAATATCTTAAAAACAAAAAGAA 932
DB 928 TGCAGTGAGTACGGCTCCACAGCAGAAACCTATAGGAAAAATATCTTAAAAACAAAAAGAA 987
QY 933 AAAAACTGAAAAAGAAAACAGAGAGGCGAGCTGAGTTATTGGAGAGCGCGCTCGAGAGAT 992
DB 988 AAAAACTGAAAAAGAAAACAGAGAGGCGAGCTGAGTTATTGGAGAGCGCGCTCGAGAGAT 1047
QY 993 AGAAGAAATTTGGACGAGAGAGCTGAAAGGAAAAATATAGAAAGAAAACATCACTCAGCTGC 1052
DB 1048 AGAAGAAATTTGGACGAGAGAGCTGAAAGGAAAAATATAGAAAGAAAACATCACTCAGCTGC 1107
QY 1053 ACCTTCCRAATACCGAGTGGCGAATACCTGCCAGAGGTGAACCTAAAAACACAGGATT 1112
DB 1108 ACCTTCCRAATACCGAGTGGCGAATACCTGCCAGAGGTGAACCTAAAAACACAGGATT 1167
QY 1113 AGAGGAGCGGCTGAGGCGAGAGACTGCAAGAGCAATGTGAAGCTGAGGACAGGAGAA 1172
DB 1168 AGAGGAGCGGCTGAGGCGAGAGACTGCAAGAGCAATGTGAAGCTGAGGACAGGAGAA 1227
QY 1173 GAAAGAAATGCTGAGAAAGAAAACATTTGAAAGAAAGATGAAGATGATGATAGTCAAGAACT 1232
DB 1228 GAAAGAAATGCTGAGAAAGAAAACATTTGAAAGAAAGATGAAGATGATGATAGTCAAGAACT 1287
QY 1233 TCGGAACATAGACCCCTACGTGGATAGAATCACCTAAACCAATGGCCCATATTGAGAAATGG 1292

DB 1288 TCGGAACATAGACCCCTACGTGGATAGAATCACCTAAAAACCAATGGCCCATATTGAGAAATGG 1347
QY 1293 CCCATTCTCAGCTGGAGCAGCAAACCTGGAACGATGAAGATGATGAAGAAAGACTGCCCAAA 1352
DB 1348 CCCATTCTCAGCTGGAGCAGCAAACCTGGAACGATGAAGATGATGAAGAAAGACTGCCCAAA 1407
QY 1353 TCCTCAGGAATAATACTTTGATGAGCCAAATGCAGAAAGTGATTACACATATATAGCAGCTC 1412
DB 1408 TCCTCAGGAATAATACTTTGATGAGCCAAATGCAGAAAGTGATTACACATATATAGCAGCTC 1467
QY 1413 CTATGAAACAAATTCATATGGTGAATTCGAAATGGACACATAAAAAATTCGCGAGTCAAGATT 1472
DB 1468 CTATGAAACAAATTCATATGGTGAATTCGCAATTCGACACATAAAAAATTCGCGAGTCAAGATT 1527
QY 1473 CCCAGAGTTTTCCACCTCGTTCTCTCTGGATCTTTAGAACCTGTGGCTCTGGGCTCTGT 1532
DB 1528 CCCAGAGTTTTCCACCTCGTTCTCTCTGGATCTTTAGAACCTGTGGCTCTGGGCTCTGT 1587
QY 1533 GCTTTCTGAGGATCACCACTTACTGAGCAAGAGGAGCAGTCCATCCCATGACAGAAAG 1592
DB 1588 GCTTTCTGAGGATCACCACTTACTGAGCAAGAGGAGCAGTCCATCCCATGACAGAAAG 1647
QY 1593 CAGAAACGGTTTCAGCCTCCAGTACTGGGGATTTGCCAAAAGCAAAAAACCCGGGCAGCTGA 1652
DB 1648 CAGAAACGGTTTCAGCCTCCAGTACTGGGGATTTGCCAAAAGCAAAAAACCCGGGCAGCTGA 1707
QY 1653 CTTGTTGTGTAATCCCTTGGATCCCGGGAATCCAGATAAAAAATTTAGAGTAAAAATTCCTGA 1712
DB 1708 CTTGTTGTGTAATCCCTTGGATCCCGGGAATCCAGATAAAAAATTTAGAGTAAAAATTCCTGA 1767
QY 1713 CTTGGGAAATGCTTTGTTGGTGCCATAAACACATTCACGGAAGACATCCAGACGGCTCAGTA 1772
DB 1768 CTTGGGAAATGCTTTGTTGGTGCCATAAACACATTCACGGAAGACATCCAGACGGCTCAGTA 1827
QY 1773 CGCTCCATAGAGTTTTTAATAGGAGCGGGTACAGACCCCTCGCGGACATCTCGGAGCAC 1832
DB 1828 CGCTCCATAGAGTTTTTAATAGGAGCGGGTACAGACCCCTCGCGGACATCTCGGAGCAC 1887
QY 1833 GCGCTGTATGGCATTTGAGCTGGCAAACGGGAGATTATTTGTTTGAACCCACATTTCTGGGGA 1892
DB 1888 GCGCTGTATGGCATTTGAGCTGGCAAACGGGAGATTATTTGTTTGAACCCACATTTCTGGGGA 1947
QY 1893 AGACTATTTCAGAGAGAGAAAGACCAATAGCCCAACATCATAGAGCTGCTAGGCAAGTATTC 1952
DB 1948 AGACTATTTCAGAGAGAGAAAGACCAATAGCCCAACATCATAGAGCTGCTAGGCAAGTATTC 2007
QY 1953 AAGGCACCTTTGCTCTATCTGGAATAATTTCTCGGAAATTTCTCAATCGCAGAGGAGAACT 2012
DB 2008 AAGGCACCTTTGCTCTATCTGGAATAATTTCTCGGAAATTTCTCAATCGCAGAGGAGAACT 2067
QY 2013 GCGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTTGTGGAAGATATGG 2072
DB 2068 GCGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTTGTGGAAGATATGG 2127
QY 2073 CTGGCCCAATGAAGATGCTGCAAGTTTACAGATTTCTCTGATCCCGATGTTGAAATGGT 2132
DB 2128 CTGGCCCAATGAAGATGCTGCAAGTTTACAGATTTCTCTGATCCCGATGTTGAAATGGT 2187
QY 2133 TCCAGAAAAACGAGCCTCAGCTGGCGAAATGCTCGGCATCTCTGGTGAATTTCTTAGCA 2192
DB 2188 TCCAGAAAAACGAGCCTCAGCTGGCGAAATGCTCGGCATCTCTGGTGAATTTCTTAGCA 2247
QY 2193 AATTCTTACCAATATTCATTTCTGAGCTAGCAAAATGTTCCAGTACATTTGGAACCTAAACGG 2252
DB 2248 AATTCTTACCAATATTCATTTCTGAGCTAGCAAAATGTTCCAGTACATTTGGAACCTAAACGG 2307
QY 2253 TGACTCTCATTTCTTAAACAGGATTAAGAGTGAAGTGGCTTTCATCTCAGACCTTTATTTT 2312
DB 2308 TGACTCTCATTTCTTAAACAGGATTAAGAGTGAAGTGGCTTTCATCTCAGACCTTTATTTT 2367
QY 2313 GCTTTGAGGTACTGTGTTTGAATTTGCTTTTGTGACATGTTGCTCTGGGAGGCT 2372

Db 2368 GCTTTGAGTACTGTGTTTGACATTTTGTGTCACACTGTGATCCTCGGGGAAGGGT 2427
Qy 2373 AGTCTTTTGTCTTACGCTAAGTAGTTTACTGACCAATTTTCTCTGGAAACAATAACATGT 2432
Db 2428 AGTCTTTTGTCTTACGCTAAGTAGTTTACTGACCAATTTTCTCTGGAAACAATAACATGT 2487
Qy 2433 CTCTAAGCATTTGTTCTTGTGTGTGTGACATTTCAAATGTCTATTTTGTGAATGAAATAAT 2492
Db 2488 CTCTAAGCATTTGTTCTTGTGTGTGTGACATTTCAAATGTCTATTTTGTGAATGAAATAAT 2547
Qy 2493 ACTTTCCCTTTGTTTGTGGCAGGTTTGTAACTATTATTAAGAAATATTTTAGCTGA 2552
Db 2548 ACTTTCCCTTTGTTTGTGGCAGGTTTGTAACTATTATTAAGAAATATTTTAGCTGA 2607
Qy 2553 GTACTATATAATTTACAATCTTAAGAAATATCAAGTTTGGGAACCAAGAAATAGCAAGG 2612
Db 2608 GTACTATATAATTTACAATCTTAAGAAATATCAAGTTTGGGAACCAAGAAATA -- GCAAG 2664
Qy 2613 GAAATGTACAAATTTTATCTTCTGGCAAAAGGACATCATTTCTCTGTATTATAGTATGTAA 2672
Db 2665 GAAATGTACAAATTTTATCTTCTGGCAAAAGGACATCATTTCTCTGTATTATAGTATGTAA 2724
Qy 2673 ATGCACCTGTAAATTTACTTTTGTGAATTAATAATGGAGGGGGAGCTCAAAATTCAGAAA 2732
Db 2725 ATGCACCTGTAAATTTACTTTTCCATTTAAATATGGGA - GGGGGACTCAAAATTTTCAGAAA 2783
Qy 2733 AGCTAAAAA 2741
Db 2784 AGCTACCAA 2792

RESULT 5

US-10-198-846-10286
; Sequence 10286, Application US/10198846
; Publication No. US2003099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: THERAPY OF BREAST CANCER
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10286
; LENGTH: 4698
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-10286

Query Match 77.9%; Score 2533.8; DB 14; Length 4698;
Best Local Similarity 99.2%; Pred. No. 0;
Matches 2568; Conservative 0; Mismatches 17; Indels 4; Gaps 2;
Qy 153 TCCGAAAAAGCCGGAGCCTCAACAGAAAGCTCTTTAGTTTCTCTCTCCACCGCCACC 212
Db 254 TTCAGAAAGCCGGAGCCTCAACAGAAAGCTCTTTAGTTTCTCTCTCCACCGCCACC 313
Qy 213 ACCACCAACCCCGCCTTTTCCGAGCCCAACCCCGGAGCAGAGAGATCCT 272
Db 314 ACCACCAACCCCGCCTTTTCCGAGCCCAACCCCGGAGCAGAGAGATCCT 373
Qy 273 GGGATCAGATGATGAGGAGCAAGGACCTCTGGGACTACTGCAAAAGGTGGATATCATCC 332
Db 374 GGGATCAGATGATGAGGAGCAAGGACCTCTGGGACTACTGCAAAAGGTGGATATCATCC 433
Qy 333 AGTGAAAAATTGGAGACCTCTTCAATGCGCGGTATCATGTTATTAGAAAGCTTGATGGGG 392

Db 434 AGTGAAAAATTGGAGACCTCTTCAATGCGCGGTATCATGTTATTAGAAAGCTTGATGGGG 493
Qy 393 GCATCTCTCTACTGTCTGGCTGTCTGGGATATGCGAGGGGAAAGATTTTGTCAATGAA 452
Db 494 GCATCTCTCTACTGTCTGGCTGTCTGGGATATGCGAGGGGAAAGATTTTGTCAATGAA 553
Qy 453 AGTTGTAAGAGTCCCGCAGCATTTATACGGAGACAGCCTTGATGAAATAAATTTGCTCAA 512
Db 554 AGTTGTAAGAGTCCCGCAGCATTTATACGGAGACAGCCTTGATGAAATAAATTTGCTCAA 613
Qy 513 ATGTGTTTCGAGAAAGTATCCAGTGACCCCAACCAAGACATGCTGTCTCCAGCTCATTTGA 572
Db 614 ATGTGTTTCGAGAAAGTATCCAGTGACCCCAACCAAGACATGCTGTCTCCAGCTCATTTGA 673
Qy 573 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTGTCATGCTTTCGAAGTACTTTGG 632
Db 674 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTGTCATGCTTTCGAAGTACTTTGG 733
Qy 633 CCACCATCTCTCTCAAGTGGATCAATCAATCAACTATCAAGGCTCCAGTACGTTGTGT 692
Db 734 CCACCATCTCTCTCAAGTGGATCAATCAATCAACTATCAAGGCTCCAGTACGTTGTGT 793
Qy 693 GAAGAGTATCATTTTCGACAGCTCTTCAAGGTTAGATTACTTACACAGTAAAGTCAAGAT 752
Db 794 GAAGAGTATCATTTTCGACAGCTCTTCAAGGTTAGATTACTTACACAGTAAAGTCAAGAT 853
Qy 753 CATTCATACCTGACATAAAGCGGAAAAATATCTTGTGATGCTGTGTGGATGATCATATGTGAG 812
Db 854 CATTCATACCTGACATAAAGCGGAAAAATATCTTGTGATGCTGTGTGGATGATCATATGTGAG 913
Qy 813 AAGAAATGGAGCTGAGGCTCTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTTCAGGGTC 872
Db 914 AAGAAATGGAGCTGAGGCTCTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTTCAGGGTC 973
Qy 932 TGCAGTGAATGAGTACGCTCCACAGCAGAAACCTTATAGGAAAAATATCTAAAAACAAAAAGAA 932
Db 974 TGCAGTGAATGAGTACGCTCCACAGCAGAAACCTTATAGGAAAAATATCTAAAAACAAAAAGAA 1033
Qy 933 AAAAATGAAAAAGAAACAGAGAGCGGCTGAGTTATTGGAGAAAGCGCTGCAAGGAGAT 992
Db 1034 AAAAATGAAAAAGAAACAGAGAGCGGCTGAGTTATTGGAGAAAGCGCTGCAAGGAGAT 1093
Qy 993 AGAAGAAATGGAGCAGAGAGCTGAAAGAAATATAGAGAAACATCACTCAGCTGC 1052
Db 1094 AGAAGAAATGGAGCAGAGAGCTGAAAGAAATATAGAGAAACATCACTCAGCTGC 1153
Qy 1053 ACCTTCCAATGACAGAGTGGCAATCTGCCAGAGGTGAAACTTAAAAACAAACAGGAT 1112
Db 1154 ACCTTCCAATGACAGAGTGGCAATCTGCCAGAGGTGAAACTTAAAAACAAACAGGAT 1213
Qy 1113 AGAGAGCGGCTGAGGCGAGAGCTGCAAGGACAAATGGTGAAGTGAAGTGAAGTGAAGTGAAG 1172
Db 1214 AGAGAGCGGCTGAGGCGAGAGCTGCAAGGACAAATGGTGAAGTGAAGTGAAGTGAAGTGAAG 1273
Qy 1173 GAAAGAAATGCTGAGAAAGAAACATTTGAAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1232
Db 1274 GAAAGAAATGCTGAGAAAGAAACATTTGAAAGATGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1333
Qy 1233 TGCAGAAATAGACCTTACGTGATGATGATCACTTAAAAACCAATGGCCCATATTGAGAAATGG 1292
Db 1334 TGCAGAAATAGACCTTACGTGATGATGATCACTTAAAAACCAATGGCCCATATTGAGAAATGG 1393
Qy 1293 CCCATTTCTCCTGAGAGCAACTGGAGCATGAAGATGATGATGAGAAAGTGAAGTGAAGTGAAG 1352
Db 1394 CCCATTTCTCCTGAGAGCAACTGGAGCATGAAGATGATGATGAGAAAGTGAAGTGAAGTGAAG 1453
Qy 1353 TCTGAGGATATATCTTGTAGTGAAGCAAAATGCAAGAAATGATTAACATATAGCAGCTC 1412
Db 1454 TCTGAGGATATATCTTGTAGTGAAGCAAAATGCAAGAAATGATTAACATATAGCAGCTC 1513
Qy 1413 CTATGAACAAATTAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1472

1514	Db	CTATGAACAATTTCAATGGTGAATTTGCCAAATGGACGACATAAAATTTCCCGAGTCCACAGTT	1571
1473	Qy	CCCAGAGTTTTTCCACCTCGTGTGTTCTCTGGATCCTTAGAAACCTGTGGCCCTCGCGCTCTGT	1532
1574	Db	CCCAGAGTTTTTCCACCTCGTGTGTTCTCTGGATCCTTAGAACCTGTGGCCCTCGCGCTCTGT	1633
1533	Qy	GCTTTCTGAGGGATCACCACTTACTGAGCAGAGGAGGAGCGATGCCATGCCATGACAGAAG	1592
1634	Db	GCTTTCTGAGGGATCACCACTTACTGAGCAGAGGAGGAGCGATGCCATGCCATGACAGAAG	1693
1593	Qy	CAGAACGGTTTTACGCTCCAGTACTGGGGATTTTGCCAAAAGCAGAAAAACCGGCGACCTGA	1652
1694	Db	CAGAACGGTTTTACGCTCCAGTACTGGGGATTTTGCCAAAAGCAGAAAAACCGGCGACCTGA	1753
1653	Qy	CTTTGTTGGTGAATCCCCTGGATCCGCGGAATGCAGATAAAATTAGAGTAAAAATTTGCTGA	1712
1754	Db	CTTTGTTGGTGAATCCCCTGGATCCGCGGAATGCAGATAAAATTAGAGTAAAAATTTGCTGA	1813
1713	Qy	CTTGGGAAATGCTTTGTTGGTGCAATAAACCTTACCGGAAGACATCCAGACGGCTCAGTA	1772
1814	Db	CCTGGGAAATGCTTTGTTGGTGCAATAAACCTTACCGGAAGACATCCAGACGGCTCAGTA	1873
1773	Qy	CCGCTCCATAGAGGTTTTAATAGAGCGGGGTACAGCACCCCTCGGACATCTCGAGCAC	1832
1874	Db	CCGCTCCATAGAGGTTTTAATAGAGCGGGGTACAGCACCCCTCGGACATCTCGAGCAC	1933
1833	Qy	GGCGTGATGGCATTTGAGCTGGCAACGGGAGATTATTGTTTGAACCAATTTCTGGGGA	1892
1934	Db	GGCGTGATGGCATTTGAGCTGGCAACGGGAGATTATTGTTTGAACCAATTTCTGGGGA	1993
1893	Qy	AGACTATTCCAGAGACGAAGACCAATAGCCCCACATCATAGAGTGTAGGCAGTATTC	1952
1994	Db	AGACTATTCCAGAGACGAAGACCAATAGCCCCACATCATAGAGTGTAGGCAGTATTC	2053
1953	Qy	AAGGCATTTGCTCTATCTGGAAAAATTTCTCGGGAATTTCTTCAATCGCAGAGGAGAACT	2012
2054	Db	AAGGCATTTGCTCTATCTGGAAAAATTTCTCGGGAATTTCTTCAATCGCAGAGGAGAACT	2113
2013	Qy	GCAGACATACACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTCTGTGAAAAGTATGG	2072
2114	Db	GCAGACATACACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTCTGTGAAAAGTATGG	2173
2073	Qy	CTGGCCCCATGAAGATGCTGCAGTTTACAGATTTCTCTGATCCCGATTTTGAAAAATGGT	2132
2174	Db	CTGGCCCCATGAAGATGCTGCAGTTTACAGATTTCTCTGATCCCGATTTTGAAAAATGGT	2233
2133	Qy	TCCGAAAAAAGAGCCCTCAGCTGGCGAATGGCTTCGCGCATCTTGGTTGAATTTCTTAGCA	2192
2234	Db	TCCGAAAAAAGAGCCCTCAGCTGGCGAATGGCTTCGCGCATCTTGGTTGAATTTCTTAGCA	2293
2193	Qy	AAATTCTACCAATATTGCAATTTCTGAGCTAGCAAAATGTTCCAGTACATTTGACACTAAACGG	2252
2294	Db	AAATTCTACCAATATTGCAATTTCTGAGCTAGCAAAATGTTCCAGTACATTTGACACTAAACGG	2353
2253	Qy	TGACTCTCATTTCTTTAAAGGATTAAGTGAAGTGAAGTGGCTTTCATCCTCAGACCTTTATTTT	2312
2354	Db	TGACTCTCATTTCTTTAAAGGATTAAGTGAAGTGAAGTGGCTTTCATCCTCAGACCTTTATTTT	2413
2313	Qy	GCTTTGAGGTACTGTTGTTTGAACATTTTGTCTTTTGTGCACTGTGATTCCTGGGGAAGGGT	2372
2414	Db	GCTTTGAGGTACTGTTGTTTGAACATTTTGTCTTTTGTGCACTGTGATTCCTGGGGAAGGGT	2473
2373	Qy	AGTCTTTTGTCTTCAGCTAAGTACTGTACTGACCATTTTCTCTCGGAAAACAAATAACATGT	2432
2474	Db	AGTCTTTTGTCTTCAGCTAAGTACTGTACTGACCATTTTCTCTCGGAAAACAAATAACATGT	2533
2433	Qy	CTCTAAGCAATGTTTCTTGTGTTGTGTGACATTCAAATGTCATTTTTTTGAATGAAAAAT	2492
2534	Db	CTCTAAGCAATGTTTCTTGTGTTGTGTGACATTCAAATGTCATTTTTTTGAATGAAAAAT	2593
2493	Qy	ACTTTCCCCTTGTGTTTTGGCAGTTTTGTAACTATTATTAGAAAAATTTTATGCTGA	2552
2594	Db	ACTTTCCCCTTGTGTTTTGGCAGTTTTGTAACTATTATTAGAAAAATTTTATGCTGA	2653

QY	2553	GTACTATATATTTACAAATCTTAAGAAATTTATCAAGTTGGGAAACCAAGAAATATGCAAGG	2612
Db	2654	GTACTATATATTTACAAATCTTAAGAAATTTATCAAGTTGGGAAACCAAGAAATA--GCAAG	2710
QY	2613	GAATGTACAAATTTTATCTCTGCGCAAGGACATCATCTCTGTATTATAGTGTATGTAA	2672
Db	2711	GAATGTACAAATTTTATCTCTGCGCAAGGACATCATCTCTGTATTATAGTGTATGTAA	2770
QY	2673	ATGCACCTGTAAATGTTTACTTTTGGATTAAATATGGGAGGGGGGACTCAAAATTTTCAGAAA	2732
Db	2771	ATGCACCTGTAAATGTTTACTTTTCCATTAAATATGGGA-GGGGGACTCAAATTTTCAGAAA	2829
QY	2733	AGCTAAAAA	2741
Db	2830	AGCTACCAA	2838
RESULT 6			
US-10-425-114-16424			
; Sequence 16424, Application US/10425114			
; Publication No. US20040034888A1			
; GENERAL INFORMATION:			
; APPLICANT: Liu, Jingdong			
; APPLICANT: Zhou, Yihua			
; APPLICANT: Kovalic, David K.			
; APPLICANT: Screen, Steven E			
; APPLICANT: Tabaska, Jack E			
; APPLICANT: Cao, Yongwei			
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with			
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement			
; FILE REFERENCE: 38-21(53313)B			
; CURRENT APPLICATION NUMBER: US/10/425,114			
; CURRENT FILING DATE: 2003-04-28			
; NUMBER OF SEQ ID NOS: 73128			
; SEQ ID NO 16424			
; LENGTH: 3699			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; OTHER INFORMATION: Clone ID: LTB3063-134-E5_FLI			
US-10-425-114-16424			

Query Match	77.7%; Score 2529; DB 16; Length 3699;
Best Local Similarity	99.4%; Pred. No. 0;
Matches 2565; Conservative	0; Mismatches 20; Indels 4; Gaps 2;
QY	153 TCGGAAAAAGCCGGAGCCTCAACAGAAAGCTCTTTAGTTCTCTCTCCACCGCCACC 212
Db	199 TTCAGAAAGCCGGAGCCTCAACAGAAAGCTCTTTAGTTCTCTCTTCACCGCCACC 258
QY	213 ACCACCAACACCGCACCTTTGCCAGACCCACACCCCGGAGCCAGAGGAGGAGATCCT 272
Db	259 ACCACCAACACCGCACCTTTGCCAGACCCACACCCCGGAGCCAGAGGAGGAGATCCT 318
QY	273 GGGATCAGATGATGAGGAGCAAGAGGACCTCGGGACTACTGCAAAAGGTGGATATCATCC 332
Db	319 GGGATCAGATGATGAGGAGCAAGAGGACCTCGGGACTACTGCAAAAGGTGGATATCATCC 378
QY	333 AGTGAAAAATTGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGGG 392
Db	379 AGTGAAAAATTGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGGG 438
QY	393 GCATCTCTACTGTCGTGGCTGTGCTGGGATATGCAGGGGAAAAGATTTTGTCGAATGAA 452
Db	439 GCATCTCTACTGTCGTGGCTGTGCTGGGATATGCAGGGGAAAAGATTTTGTCGAATGAA 498
QY	453 AGTTGTAAAAAGTGCCACGATTTATACGGAGACAGCCTTGCATGAAATAAAATTGCTCAA 512
Db	499 AGTTGTAAAAAGTGCCACGATTTATACGGAGACAGCCTTGGATGAAATAAAATTGCTCAA 558
QY	513 ATGTGTTTCGAGAAAGTGATCCCAAGTACCCAAACAAAGACATGGTGGTCAGCTCATTTGA 572

Db 559 ATGTGTTTCGAGAAAGTGTATCCAGTGACCCAAACAAAGACATGTTGGTCCAGCTCAITGA 618
Qy 573 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTGCGATGCTCTTCGAGTACTTGG 632
Db 619 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTGCGATGCTCTTCGAGTACTTGG 678
Qy 633 CCACCATCTCTCAAGTGGATCATCAAAATCOAACTATCAAGGCCTCCAGTACGTTGTGT 692
Db 679 CCACCATCTCTCAAGTGGATCATCAAAATCOAACTATCAAGGCCTCCAGTACGTTGTGT 738
Qy 693 GAAGAGTATCAITTCGACAGGTCCTTCAAGGGTTAGATTAATTACACAGTAAGTGAAGAT 752
Db 739 GAAGAGTATCAITTCGACAGGTCCTTCAAGGGTTAGATTAATTACACAGTAAGTGAAGAT 798
Qy 753 CATTCATCTGACATAAAGCCGGAAATATCTTGATGTGTGTGGATGATGATATGTGAG 812
Db 799 CATTCATCTGACATAAAGCCGGAAATATCTTTATGTGTGTGGATGATGATATGTGAG 858
Qy 813 AAGAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTTCAGGGTC 872
Db 859 AAGAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTTCAGGGTC 918
Qy 873 TGCAGTGTAGTACGGCTCCACAGCAGAAACCTATAGGAAATATCTTAAACAAAGAA 932
Db 919 TGCAGTGTAGTACGGCTCCACAGCAGAAACCTATAGGAAATATCTTAAACAAAGAA 978
Qy 933 AAAAATGAAAAGAAACAGAGGCGAGCTGAGTTATTTGGAGAGCGCTGCAGGAT 992
Db 979 AAAAATGAAAAGAAACAGAGGCGAGCTGAGTTATTTGGAGAGCGCTGCAGGAT 1038
Qy 993 AGAAGAAATTTGGAGCAGAGAGCTGAAAGGAAATATAGAGAAACCATCACTCAGCTGC 1052
Db 1039 AGAAGAAATTTGGAGCAGAGAGCTGAAAGGAAATATAGAGAAACCATCACTCAGCTGC 1098
Qy 1053 ACCTTCCAATGACAGGATGGGGAATACCTGCCAGAGGTGAACTTAAACAAAGAGAT 1112
Db 1099 ACCTTCCAATGACAGGATGGGGAATACCTGCCAGAGGTGAACTTAAACAAAGAGAT 1158
Qy 1113 AGAGGAGCGGCTGAGCAGAGAGCTCAAGAGCAATGTTGAAGCTGAGGACAGGAAAGA 1172
Db 1159 AGAGGAGCGGCTGAGCAGAGAGCTCAAGAGCAATGTTGAAGCTGAGGACAGGAAAGA 1218
Qy 1173 GAAAGAGATGCTTGAGAAAGAAACATTTGAAAGATGAAGATGATGATGATGAGAACT 1232
Db 1219 GAAAGAGATGCTTGAGAAAGAAACATTTGAAAGATGAAGATGATGATGATGAGAACT 1278
Qy 1233 TGGCAATAGACCTTACGTGGATAGAAATCACTTAAACCAATGGCCATATTGAGAACTG 1292
Db 1279 TGGCAATAGACCTTACGTGGATAGAAATCACTTAAACCAATGGCCATATTGAGAACTG 1338
Qy 1293 CCCATCTCACTGGAGCAGCACTGGACGATGAAGATGATGATGAAGAGACTGCCCCAA 1352
Db 1339 CCCATCTCACTGGAGCAGCACTGGACGATGAAGATGATGATGAAGAGACTGCCCCAA 1398
Qy 1353 TCCTGAGGAATAAATCTTGATGAGCCAAATGAGAAAGTGAATACATATAGAGCTC 1412
Db 1399 TCCTGAGGAATAAATCTTGATGAGCCAAATGAGAAAGTGAATACATATAGAGCTC 1458
Qy 1413 CTATGAACAAATCAATGGTGAATGGCAATGACGACATAAATTTCCGAGTCAAGTT 1472
Db 1459 CTATGAACAAATCAATGGTGAATGGCAATGACGACATAAATTTCCGAGTCAAGTT 1518
Qy 1473 CCCAGAGTTTCCACCTCGTTGTTCTCTGATCTCTGATCTCTGATCTCTGATCTCTG 1532
Db 1519 CCCAGAGTTTCCACCTCGTTGTTCTCTGATCTCTGATCTCTGATCTCTGATCTCTG 1578
Qy 1533 GCTTCTGAGGATACCACTTACTGAGCAAGAGGAGCAGTCCATCCCATGACAGAG 1592
Db 1579 GCTTCTGAGGATACCACTTACTGAGCAAGAGGAGCAGTCCATCCCATGACAGAG 1638
Qy 1593 CAGAACCGTTTACGCTCCAGTACTCGGGGATTTGCCAAAGGCAAAACCCGGGAGCTGA 1652
Db 1639 CAGAACCGTTTACGCTCCAGTACTCGGGGATTTGCCAAAGGCAAAACCCGGGAGCTGA 1698

Qy 1653 CTTGTTGGTGAATCCCTCGATCCGCGAATGCGAATAAAATTAGAGTAAAAATTCGTGA 1712
Db 1699 CTTGTTGGTGAATCCCTCGATCCGCGAATGCGAATAAAATTAGAGTAAAAATTCGTGA 1758
Qy 1713 CTTGCGGAAATCTGTTGGTGCATAAACAATTCACGGAGACATCCAGACGCTCAGTA 1772
Db 1759 CTTGCGGAAATCTGTTGGTGCATAAACAATTCACGGAGACATCCAGACGCTCAGTA 1818
Qy 1773 CCGCTCCATAGAGGTTTAAATAGGAGCGGGTACAGCACCCCTGCGGACATCTGGAGCAC 1832
Db 1819 CCGCTCCATAGAGGTTTAAATAGGAGCGGGTACAGCACCCCTGCGGACATCTGGAGCAC 1878
Qy 1833 GCGGTGTATGGCATTTGAGCTGGCAACGGGAGATTAATTTGTTGAAACCAATCTCTGGGGA 1892
Db 1879 GCGGTGTATGGCATTTGAGCTGGCAACGGGAGATTAATTTGTTGAAACCAATCTCTGGGGA 1938
Qy 1893 AGACTATTCAGAGACGAAACACATAGCCCAATCATAGAGCTGCTAGGCAATATTC 1952
Db 1939 AGACTATTCAGAGACGAAACACATAGCCCAATCATAGAGCTGCTAGGCAATATTC 1998
Qy 1953 AAGCACTTTGCTCTATCTGAAAAATATCTCGGGAATTTCTCAATCGCAGAGAGAACT 2012
Db 1999 AAGCACTTTGCTCTATCTGAAAAATATCTCGGGAATTTCTCAATCGCAGAGAGAACT 2058
Qy 2013 GCGACATCAACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTATCTTGTGAAAAAGTATGG 2072
Db 2059 GCGACATCAACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTATCTTGTGAAAAAGTATGG 2118
Qy 2073 CTGCCCCCATGAAAGTCTGCACAGTTTACAGATTTCTCTGATCCGATGTTAGAAAAATGGT 2132
Db 2119 CTGCCCCCATGAAAGTCTGCACAGTTTACAGATTTCTCTGATCCGATGTTAGAAAAATGGT 2178
Qy 2133 TCCAGAAAAACGAGCCTCAGCTGGCGAATGCTTCGCAATGCTTCGCAATGCTTCGCAATGCTTCGCA 2192
Db 2179 TCCAGAAAAACGAGCCTCAGCTGGCGAATGCTTCGCAATGCTTCGCAATGCTTCGCAATGCTTCGCA 2238
Qy 2193 AATTCACCAATATTTGATCTGAGCTAGCAAAATGTTCCAGATCAATTTGGACCTTAAACGG 2252
Db 2239 AATTCACCAATATTTGATCTGAGCTAGCAAAATGTTCCAGATCAATTTGGACCTTAAACGG 2298
Qy 2253 TGACTCTCATTTTAAACAGGATTAACAGTGAAGTGGCTTCATCTCAGACCTTTATTTT 2312
Db 2299 TGACTCTCATTTTAAACAGGATTAACAGTGAAGTGGCTTCATCTCAGACCTTTATTTT 2358
Qy 2313 GCTTTGAGGTACTGTTGTTGCAATTTGCTTTTGTGCACTGTGATCCTGGGGAAGGTT 2372
Db 2359 GCTTTGAGGTACTGTTGTTGCAATTTGCTTTTGTGCACTGTGATCCTGGGGAAGGTT 2418
Qy 2373 AGTCTTTTGTCTTCAAGTAACTGTTTACCAATTTTCTTGGAAACCAATTAACATGT 2432
Db 2419 AGTCTTTTGTCTTCAAGTAACTGTTTACCAATTTTCTTGGAAACCAATTAACATGT 2478
Qy 2433 CTCTAAGCATTTCTTGTGTGTGTGTCATTTCAAATGTCATTTTGTGAATGAAAAAT 2492
Db 2479 CTCTAAGCATTTCTTGTGTGTGTGTCATTTCAAATGTCATTTTGTGAATGAAAAAT 2538
Qy 2493 ACTTTCCCTTTGTTTTGGCAGGTTTGTAACTAATTTATGAAGAAATATTTAGCTGA 2552
Db 2539 ACTTTCCCTTTGTTTTGGCAGGTTTGTAACTAATTTATGAAGAAATATTTAGCTGA 2598
Qy 2553 GTACTATATAATTTAAATCTTAAAGAAATTTCAAGTTGGGAACCAAGAAATAGCAAGG 2612
Db 2599 GTACTATATAATTTAAATCTTAAAGAAATTTCAAGTTGGAAACCAAGAAATA--GCAAG 2655
Qy 2613 GAAATGTACAAATTTTATCTTGGCAAGGGAACATCATCTCTGTATTTATGTGTATGTAA 2672
Db 2656 GAAATGTACAAATTTTATCTTGGCAAGGGAACATCATCTCTGTATTTATGTGTATGTAA 2715
Qy 2673 ATGCAACCTGTAAATTTACTTTTGAATTAATATGGAGGGGGAGCTCAAAATTTTCAAGAAA 2732
Db 2716 ATGCAACCTGTAAATTTACTTTTCCATTTAAATATGGGA--GGGGAGCTCAAAATTTTCAAGAAA 2774

QY 2733 AGCTAAAAA 2741
Db 2775 AGCTACCAA 2783

RESULT 7
US-09-981-397A-21
; Sequence 21, Application US/09981397A
; Publication No. US20030082519A1
; GENERAL INFORMATION:
; APPLICANT: Axxima Pharmaceuticals AG
; APPLICANT: Schubart, Daniel
; APPLICANT: Habenberger, Peter
; APPLICANT: Stein-Gerlach, Matthias
; APPLICANT: Bevec, Dorian
; TITLE OF INVENTION: Cellular Kinases Involved in Cytomegalovirus Infection and their
; FILE REFERENCE: AXM-004.1 US
; CURRENT APPLICATION NUMBER: US/09/981,397A
; CURRENT FILING DATE: 2002-06-28
; PRIOR FILING DATE: 2000-10-16
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 3745
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-397A-21

Query Match 76.8%; Score 2497; DB 10; Length 3745;
Bseq Local Similarity 98.8%; Pred. No. 0;
Matches 2559; Conservative 0; Mismatches 20; Indels 10; Gaps 4;

QY 153 TCCGAAAAACCGGAGCCCTCAACAGAAAGCTCTCTTAGTTCCTCTCTCTCCACCGCCACC 212
Db 217 TTCAGAAAGCCGGAGCCTCAACAGAAAGCTCTCTTAGTTCCTCTCTCCACCGCCACC 276

QY 213 ACCACACACCCGACCTTTGCCAGACCCCAACCCCGGAGCCAGAGGAGATCCT 272
Db 277 ACCACACCCGACCTTTGCCAGACCCCAACCCCGGAGCCAGAGGAGATCCT 336

QY 273 GGGATCAGATGATGAGGACAGAGACCCCTCGGACTACTCCAAAGGTGGATATCATCC 332
Db 337 GGGATCAGATGATGAGGACAGAGACCCCTCGGACTACTCCAAAGGTGGATATCATCC 396

QY 333 AGTGAATAATGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 392
Db 397 AGTGAATAATGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 456

QY 393 GCACCTTCTACTGTCTGCTGTGCTGGGATATGAGGGGAAAAAGATTGTTGCAATGAA 452
Db 457 GCACCTTCTACTGTCTGCTGTGCTGGGATATGAGGGGAAAAAGATTGTTGCAATGAA 516

QY 453 AGTTGTAATAAGTGGCCAGCATATACGAGACAGCTTGGATGAAATAAAATTCGTCNA 512
Db 517 AGTTGTAATAAGTGGCCAGCATATACGAGACAGCTTGGATGAAATAAAATTCGTCNA 576

QY 513 ATGTGTTCGAGAAAGTGATCCAGTGACCCCAACAAAGACATGGTGGTCCAGCTCATGA 572
Db 577 ATGTGTTCGAGAAAGTGATCCAGTGACCCCAACAAAGACATGGTGGTCCAGCTCATGA 636

QY 573 CGACTTCAAGATTTCAGGCATGAATGGGATACATGTCTGCATGTGTTCCGAAAGTACTGG 632
Db 637 CGACTTCAAGATTTCAGGCATGAATGGGATACATGTCTGCATGTGTTCCGAAAGTACTGG 696

QY 633 CCACATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCCAAGTACGTTGGT 692
Db 697 CCACATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCCAAGTACGTTGGT 756

QY 693 GAAGAGTATCATTCGACAGCTCTTCAAGGGTTAGTTACTTACACAGTAAGTGAAGAT 752
Db 757 GAAGAGTATCATTCGACAGCTCTTCAAGGGTTAGTTACTTACACAGTAAGTGAAGAT 816

QY 753 CATTCATCTACATAAAGCCGGAAAAATATCTTGATGTGTGGATGATGCATATGTGAG 812
Db 817 CATTCATCTACATAAAGCCGGAAAAATATCTTGATGTGTGGATGATGCATATGTGAG 876

QY 813 AAGAATGCGAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCTCCGGGTC 872
Db 877 AAGAATGCGAGCTGAG---CCTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCTCCGGGTC 933

QY 873 TGCAGTGTAGTACGGCTCCACAGCAGAAACCTATAGGAAAAATATCTTAAAAACAAAAAGAA 932
Db 934 TGCAGTGTAGTACGGCTCCACAGCAGAAACCTATAGGAAAAATATCTTAAAAACAAAAAGAA 993

QY 933 AAAACTGAAAAAGAAACAGAGAGCAGCGCTGAGTTATTGGAGAGCGGCTCGAGAGAT 992
Db 994 AAAACTGAAAAAGAAACAGAGAGCAGCGCTGAGTTATTGGAGAGCGGCTCGAGAGAT 1053

QY 993 AGAAGAATTGGAGCGAGAAAGCTGAAAGGAAAAATATAGAGAAAAACATCACCTCAGCTGC 1052
Db 1054 AGAAGAATTGGAGCGAGAAAGCTGAAAGGAAAAATATAGAGAAAAACATCACCTCAGCTGC 1113

QY 1053 ACCTTCCAATGACCAAGGATGGCGAATACTGCCCAGAGGTGAAACTTAAAAACAAACAGGATT 1112
Db 1114 ACCTTCCAATGACCAAGGATGGCGAATACTGCCCAGAGGTGAAACTTAAAAACAAACAGGATT 1173

QY 1113 AGAGGAGCGGCTGAGGCGAGAGACTGCAAAAGGACAAATGGTGAAGCTGAGGACACAGGAAGA 1172
Db 1174 AGAGGAGCGGCTGAGGCGAGAGACTGCAAAAGGACAAATGGTGAAGCTGAGGACACAGGAAGA 1233

QY 1173 GAAAGAAGATGCTGAGAAAGAAAAACATTTGAAAAAGATGAAGATGATGTAGATCAGGAAC 1232
Db 1234 GAAAGAAGATGCTGAGAAAGAAAAACATTTGAAAAAGATGAAGATGATGTAGATCAGGAAC 1293

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Db 1294 TGCGAAACATAGACCCCTAGCTGATAGAATCACCTTAAACCAATGGCCATATTGAGAAATGG 1353

QY 1293 CCCATTCTCAGTGGAGCAGCAACTGGACGATGAAGATGATGAAGAAAGACTGCCCAAA 1352
Db 1354 CCCATTCTCAGTGGAGCAGCAACTGGACGATGAAGATGATGAAGAAAGACTGCCCAAA 1413

QY 1353 TCCTCAGGAATATATCTTGATGAGCCAAATGCAAAAGTGAATACACATATAGCAGCTC 1412
Db 1414 TCCTCAGGAATATATCTTGATGAGCCAAATGCAAAAGTGAATACACATATAGCAGCTC 1473

QY 1413 CTATGAAACAATTCATGTGTGAATTCGCAATGGACGACATAAAATTCGCGAGTCAAGATT 1472
Db 1474 CTATGAAACAATTCATGTGTGAATTCGCAATGGACGACATAAAATTCGCGAGTCAAGATT 1533

QY 1473 CCCAGAGTTTCCACCTCGTTGTTCTCTGGATCTCTAGAACTGTGGCTCGCGGCTCTGT 1532
Db 1534 CCCAGAGTTTCCACCTCGTTGTTCTCTGGATCTCTAGAACTGTGGCTCGCGGCTCTGT 1593

QY 1533 GCTTCTCAGGGATCACCACTTACTGAGCAGAGAGAGAGAGCTCCATCCCATGACAGAG 1592
Db 1594 GCTTCTCAGGGATCACCACTTACTGAGCAGAGAGAGAGAGCTCCATCCCATGACAGAG 1653

QY 1593 CAGAACGGTTTCAGGCTCCAGTACCTGGGATTTGCAAAAGCAAAACCCGGGCGCTGCA 1652
Db 1654 CAGAACGGTTTCAGGCTCCAGTACCTGGGATTTGCAAAAGCAAAACCCGGGCGCTGCA 1713

QY 1653 CTTGTTGTGTAATCCCTTGGATCCCGGAAATGCAAGTAAAAATTAGAGTAAAAATTGCTGA 1712
Db 1714 CTTGTTGTGTAATCCCTTGGATCCCGGAAATGCAAGTAAAAATTAGAGTAAAAATTGCTGA 1773

QY 1713 CCTGGAAATGCTGTTGGGTGCATAACATTTACGAGNAGACATCCAGACCGGCTCAGTA 1772
Db 1774 CCTGGAAATGCTGTTGGGTGCATAACATTTACGAGNAGACATCCAGACCGGCTCAGTA 1833

QY 1773 CGCTCCCATAGAGTTTAAATAGGAGCGGGGTACAGACCCCTCGGGACATCTGGAGCAC 1832
Db 1834 CGCTCCCATAGAGTTTAAATAGGAGCGGGGTACAGACCCCTCGGGACATCTGGAGCAC 1893

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QY 1833 GCGGTGATGCAATTTGAGCTGGCAACGGGAGATTATTTGTTGAAACACATTTCTGGGA 1892
Db 1894 GCGGTGATGCAATTTGAGCTGGCAACGGGAGATTATTTGTTGAAACACATTTCTGGGA 1953
QY 1893 AGACTATTCCAGAGACGAAGACCCACATAGAGCTGCTAGGACGATATCC 1952
Db 1954 AGACTATTCCAGAGACGAAGACCCACATAGAGCTGCTAGGACGATATCC 2013
QY 1953 AAGGACATTTGCTCTATCTGGAATAATTTCTCGGGAATTTCTCAATCGCAGAGAACT 2012
Db 2014 AAGGACATTTGCTCTATCTGGAATAATTTCTCGGGAATTTCTCAATCGCAGAGAACT 2073
QY 2072 GCGACACATCACAGCTGAGCCCTGGAGCTCTTTGATGCTACTGTTGGGAAAGTATGG 2072
Db 2074 GCGACACATCACAGCTGAGCCCTGGAGCTCTTTGATGCTACTGTTGGGAAAGTATGG 2133
QY 2073 CTGGCCCATGAAGATGCTGCACAGTTTACAGATTTCTGATCCCGATGTTAGAAATGGT 2132
Db 2134 CTGGCCCATGAAGATGCTGCACAGTTTACAGATTTCTGATCCCGATGTTAGAAATGGT 2193
QY 2133 TCCAGAAAACGAGCTCAGCTGGCGAATGCTTCGGCATCCTTGTTGAAATTTCTTAGCA 2192
Db 2194 TCCAGAAAACGAGCTCAGCTGGCGAATGCTTCGGCATCCTTGTTGAAATTTCTTAGCA 2250
QY 2193 AATTCTACCAATATTGCAATTTCTGAGCTAGCAAAATGTTCCAGTACATTTGGACCTAAACGG 2252
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QY 2253 TGACTCTCATTTTAAACAGGATTTACAGTGAAGCTGGCTTCACTCTGAGACCTTTATTTT 2312
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QY 2313 GCTTTGAGTACTGTTGTTTGGACATTTGTTGTCACATGTCATCTCTGGGGAAGGT 2372
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QY 2373 AGTCTTTTGTCTTCAGCTAAGTAGTTTACTGACCAATTTTCTCTGGAACAAATACATGT 2432
Db 2431 AGTCTTTTGTCTTCAGCTAAGTAGTTTACTGACCAATTTTCTCTGGAACAAATACATGT 2490
QY 2433 CTCTAAGCATGTTTCTGTTGTTGTCACATTTCAATGTCATTTTGAATGAAAT 2492
Db 2491 CTCTAAGCATGTTTCTGTTGTTGTCACATTTCAATGTCATTTTGAATGAAAT 2550
QY 2493 ACTTTCCCTTTGTTTGGCAGGTTTGTAACTATTTATGAAGAAATATTTTACTGTA 2552
Db 2551 ACTTTCCCTTTGTTTGGCAGGTTTGTAACTATTTATGAAGAAATATTTTACTGTA 2610
QY 2553 GTACTATATAATTTAACTTTAAGAAATTTCAAGTTGGGAACCAAGAAATAGCAAGG 2612
Db 2611 GTACTATATAATTTAACTTTAAGAAATTTCAAGTTGGGAACCAAGAAATA 2667
QY 2613 GAAATGTACAAATTTTATCTTCGCAAGGACATCATTTCTGTTATATAGTGTATGTA 2672
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QY 2673 ATGCACCTGTAATTTGTTTACTTTGATTAATATGGAGGGGACTCAAAATTCAGAAA 2732
Db 2728 ATGCACCTGTAATTTGTTTACTTTCCATTAATATGGA -GGGGGACTCAAAATTCAGAAA 2786
QY 2733 AGCTAAAAA 2741
Db 2787 AGCTACCAA 2795
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RESULT 8
US-09-759-359A-3
; Sequence 3, Application US/09759359A
; Patent No. US20020094560A1
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEN, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

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; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001043  
; CURRENT APPLICATION NUMBER: US/09/759,359A  
; CURRENT FILING DATE: 2001-01-16  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 90541  
; TYPE: DNA  
; ORGANISM: Human  
US-09-759-359A-3  
  
Query Match 20.5%; Score 666.2; DB 9; Length 90541;  
Best local Similarity 97.3%; Pred. No. 2.5e-147;  
Matches 721; Conservative 0; Mismatches 13; Indels 7; Gaps 4;  
  
QY 2004 AGGAGAACTCGGACACATCACCAAGCTGAAGCCCTCGAGGCTCTTTGATGCTACTTGTGGA 2063  
Db 87810 AGGAGAACTCGGACACATCACCAAGCTGAAGCCCTCGAGGCTCTTTGATGCTACTTGTGGA 87869  
QY 2064 AAAGTATGGCTGGCCCCCATGAAGATGCTGCACAGTTTACAGATTTCTGATCCCGATGTT 2123  
Db 87870 AAAGTATGGCTGGCCCCCATGAAGATGCTGCACAGTTTACAGATTTCTGATCCCGATGTT 87929  
QY 2124 AGAAATGGTTCCAGAAAACGAGCCTCAGCTGGCGAATGCTTCGGCATCCTTTGGTGTGAA 2183  
Db 87930 AGAAATGGTTCCAGAAAACGAGCCTCAGCTGGCGAATGCTTCGGCATCCTTTGGTGTGAA 87989  
QY 2184 TTCTTAGCAATTTCTACCAATATTGCAATTTCTGAGCTAGCAAAATGTTCCAGTACATTTGGA 2243  
Db 87990 TTCTTAGCAATTTCTACCAATATTGCAATTTCTGAGCTAGCAAAATGTTCCAGTACATTTGGA 88049  
QY 2244 CCTAAACGGTGACTCTCATTTCTTTAAACAGGATTTACAGTGAAGCTGGCTTCACTCTCAGAC 2303  
Db 88050 CCTAAACGGTGACTCTCATTTCTTTAAACAGGATTTACAGTGAAGCTGGCTTCACTCTCAGAC 88109  
QY 2304 CTTTATTTTGGTTGAGTACTGTTGTTGACATTTTGTGCTTTTGTGCTACTGTGATCCTG 2363  
Db 88110 CTTTATTTTGGTTGAGTACTGTTGTTGACATTTTGTGCTTTTGTGCTACTGTGATCCTG 88169  
QY 2364 GGGAAAGGTAGTCTTT -TGCTTTACAGTAAAGTATTTAGTACCATTTTCTTCTCGAA 2420  
Db 88170 GGGAAAGGTAGTCTTTTGTGTTTGTGCTTACAGTAAAGTATTTAGTACCATTTTCTTCTCGAA 88229  
QY 2421 ACAATACATGCTCTTAAGCAATGTTTCTGTTGTTGTCACATTTCAAAATGCTCATTTT 2480  
Db 88230 ACAATACATGCTCTTAAGCAATGTTTCTGTTGTTGTCACATTTCAAAATGCTCATTTT 88289  
QY 2481 TGAATGAAAAATACTTTTCCCTTTTGTGTTTGGCAGGTTTGTAACTATTTTATCAAGAA 2540  
Db 88290 TGAATGAAAAATACTTTTCCCTTTTGTGTTTGGCAGGTTTGTAACTATTTTATCAAGAA 88349  
QY 2541 TATTTAGCTAGTACTATATAATTTCAATCTTAAGAAATATCAAGTTGGGACCAAG 2600  
Db 88350 TATTTAGCTAGTACTATATAATTTCAATCTTAAGAAATATCAAGTTGGGACCAAG 88409  
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Db 88410 AATA ---GCAAGGAAATGTCAAATTTTATCTTCGCAAGGACATCATTTCTCTGTATTA 88466  
QY 2661 TAGTGTATGTAATGACCCCTGTAAATGTTTCTTTGATTTAAATATGGAGGGGGGACTC 2720  
Db 88467 TAGTGTATGTAATGACCCCTGTAAATGTTTCTTTGATTTAAATATGGAGGGGGGACTC 88525  
QY 2721 AAATTTCAAGAAAGCTAAAAA 2741  
Db 88526 AAATTTCAAGAAAGCTAAAAA 88546
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RESULT 9
US-10-207-973-3
; Sequence 3, Application US/10207973
; Publication No. US20030175927A1

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; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/10/207,973
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-10-207-973-3

Query Match      20.5%; Score 666.2; DB 15; Length 90541;
Best Local Similarity 97.3%; Pred. No. 2.5e-147;
Matches 721; Conservative 0; Mismatches 13; Indels 7; Gaps 4;

QY 2004 AGGAGAACTGCGACACATCACCAGCTGAAGCCCTGGAGCCCTTTGATGACTTGTGGA 2063
DB 87810 AGGAGAACTGCGACACATCACCAGCTGAAGCCCTGGAGCCCTTTGATGACTTGTGGA 87869

QY 2064 AAGATATGGCTGGCCCATGAAGATGCTGCACAGTTTACAGATTTCCCTGATCCCGATGTT 2123
DB 87870 AAGATATGGCTGGCCCATGAAGATGCTGCACAGTTTCCCTGATCCCGATGTT 87929

QY 2124 AGAAATGGTTCCAGAAAAACGAGCCCTCAGCTGGCGAATGCCCTTCGGCATCCTTGGTGAA 2183
DB 87930 AGAAATGGTTCCAGAAAAACGAGCCCTCAGCTGGCGAATGCCCTTCGGCATCCTTGGTGAA 87989

QY 2184 TTCTTAGCAAAATCTACCAATATGCAATCTGAGCTAGCAAAATGTTCCAGTACATTTGGA 2243
DB 87990 TTCTTAGCAAAATCTACCAATATGCAATCTGAGCTAGCAAAATGTTCCAGTACATTTGGA 88049

QY 2244 CCTAAACGGTGACTCTCTCAATCTTTAAACAGGATTTACAAGTGAGCTGGCTTCCTCAGAC 2303
DB 88050 CCTAAACGGTGACTCTCTCAATCTTTAAACAGGATTTACAAGTGAGCTGGCTTCCTCAGAC 88109

QY 2304 CTTTATTTTGGCTTTCAGGTAAGTCTGTTTGAACATTTTGGTTCGCACTGTGATCCTG 2363
DB 88110 CTTTATTTTGGCTTTCAGGTAAGTCTGTTTGAACATTTTGGTTCGCACTGTGATCCTG 88169

QY 2364 GGGAGGGTAGTCTTTT--TGCTTTCAGCTAGTACTGTTTACTGACCATTTTCTT-CTGGAA 2420
DB 88170 GGGAGGGTAGTCTTTTGGTGTCTTACAGCAATGTTTCTGAGCAATTTTCTTCTGGAA 88229

QY 2421 ACAATAACATGTCTCTAAGCAATTTGTTTCTTGTGTTGTGACATTTCAATGTCAATTTT 2480
DB 88230 ACAATAACATGTCTCTAAGCAATTTGTTTCTTGTGTTGTGACATTTCAATGTCAATTTT 88289

QY 2481 TGAATGAAAAATACATTTCCCTTGGTGTGTTGGCAGGTTTGTAACTATTATGAAGAA 2540
DB 88290 TGAATGAAAAATACATTTCCCTTGGTGTGTTGGCAGGTTTGTAACTATTATGAAGAA 88349

QY 2541 TATTTTAGCTAGTACTATATAATTTACAATCTTAAGAAATTTACAAGTTGGGAACCAAG 2600
DB 88350 TATTTTAGCTAGTACTATATAATTTACAATCTTAAGAAATTTACAAGTTGGGAACCAAG 88409

QY 2601 AAAATAGCAAGGAAATGTACAAATTTTATCTTCTGCAAGGAGGACATCATTTCTGTATTA 2660
DB 88410 AAAATAGCAAGGAAATGTACAAATTTTATCTTCTGCAAGGAGGACATCATTTCTGTATTA 88466

QY 2661 TAGTGTATGTAATGACCCCTGTAATGTTTACTTTTGGATTAATATATGGAGGGGGGACTC 2720
DB 88467 TAGTGTATGTAATGACCCCTGTAATGTTTACTTTTGGATTAATATATGGAGGGGGGACTC 88525

QY 2721 AAATTTTCAGAAAAGCTTAAAA 2741
DB 88526 AAATTTTCAGAAAAGCTTAAAA 88546
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Db 88467 TAGTGTATGTAATGCACCTGTAAATGTACTTTCCATTAAATATGGGA-GGGGACTC 88525
Qy 2721 AAATTTTCAGAAAAGCTAAAAA 2741
Db 88526 AAATTTTCAGAAAAGCTACCAA 88546

RESULT 11
US-09-880-107-3294
; Sequence 3294, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3294
; LENGTH: 4326
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U09564
US-09-880-107-3294

Query Match 19.5%; Score 632.8; DB 9; Length 4326;
Best Local Similarity 60.4%; Pred. No. 3.5e-140;
Matches 1172; Conservative 0; Mismatches 672; Indels 96; Gaps 4;

Qy 250 CCGGAGCCAGAGAGAGATCTGGGATCAGATGATGAGGACCAAGAGACCCCTCGGAC 309
Db 232 CCAGAGCAGAAAGAGAGATCTGGGATCTGATGATGAGCAGAGAGATCTTAATGAT 291
Qy 310 TACTGCAAAAGGTGGATATCATCCAGTGAATAATGGAGACCTCTTCAATGGCCGGTATCAT 369
Db 292 TATTGTAAAGGAGGTATCATCTTGTGAAAATTTGGAGATCTATTCAATGGGAGATACCAT 351
Qy 370 GTTATTAGAAAGCTTGGATGGGGACCTTCTACTGTCTGGCTGTCTGGGATATGAG 429
Db 352 GTGATCCGAAAGTTAGGCTGGGGACACTTTTCAACAGTATGGTTATCATGGGATATTCAG 411
Qy 430 GGGAAAAGATTTGTTGCAATGAAAGTTGTAAAAAGTGGCCAGCATTTATACGGAGACAGCC 489
Db 412 GGGAGCAAAATTTGTGGCAATGAAGTAGTAAAGTGTGTAACATTTACTGTAACAGCA 471
Qy 490 TTGGATGAAATAAAATTTGCTCAAAATGTGTTCCAGAAAGTATCCAGATGACCCCAACAAA 549
Db 472 CTAGATGAAATCCGGTTGCTGAAGTCAGTTGCAATTCAGACCCCTAATGATCCAAATAGA 531
Qy 550 GACATGGTGGTCAGCTCATTCAGCACTTCAGATTTTCAGGATGATGATGATGATGATGATG 609
Db 532 GAAATGGTTGTTCAACTACTAGTACATTTTAAATATATCAGGAGTTAATGGAAACATATC 591
Qy 610 TGCATGGTCTCAGAGTACTTGGCCACCATCTCTCAAGTGGATCATCAAAATCCAACTAT 669
Db 592 TGCATGGTATTTGAAGTTTGGGCAATCATCTGCTCAAGTGGATCATCAAAATCCAACTAT 651
Qy 670 CAAGGCTCCAGTACGTTGTGTAAGAGTATCATTTGCAAGGTCCTTCAAGGGTTAGAT 729
Db 652 CAGGGCTTCCACTGGCTTGTGTCAAAAAAATTTATTCAGCAAGTGTGTACAGGGTCTTGAT 711
Qy 730 TACTTACAGTAAGTGCAGATCATTTACTATGACATTAAGCCGGAATAATCTTGATG 789

Db 712 TATTTCATCAATCAAGTCCCGTATCATCCACTGACATTTAAACCAGAGAACATCTTATTG 771
Qy 790 TGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 849
Db 772 TCAGTGAATGAGCAGTACATTTCCGAGGCTGGTCGAGAAGCAACAGAAATGGCAGCATCT 831
Qy 850 GGTGCT 909
Db 832 GGAGCT 891
Qy 910 AAAATATCTAAAAACAAAAAGAAAAAATGAAAAAGAAAAACAGAAAGAGAGAGAGAGAGTGA 969
Db 892 AAAATGTCAAAGATAAAGAAAGAAATTTGAAGAAAGAAAGAAAGAGAGAGAGAGAGAGTGA 951
Qy 970 TTGAG 1029
Db 952 CTAG 997
Qy 1030 GAAGAAAAATCATCCTCAGCTGACCTTCCATGACAGAGATGGGATGATGATGATGATGATG 1089
Db 998 -----GCCCTGGGCAAAAAAGACCAAAAC 1020
Qy 1090 GTGAAATCTAAAAACAACAGAGATTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1149
Db 1021 AAGCAAGAGAGATCAGAGAGATCTCTGTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
Qy 1150 GGTGAAGCTGAT 1209
Db 1081 ATGACCCCAAGAAAAAATTTGAAGAGTCAAGTACCATTTGGCCAGGATCAAACTTATGGA 1140
Qy 1210 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1269
Db 1141 CGTGATACAGAT 1200
Qy 1270 ACCAATGGCCATATTGAGATGGCCCATTTCTACTGGAGAGAGAGAGAGAGAGAGAGAGAT 1329
Db 1201 TATCTCGAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
Qy 1330 GATGATGAG 1389
Db 1261 GACTGTGATGTCAAAAATTTGAATCAGGAATCTAGTTTCTTAAAGTCTCTCCAAATGGAGA- 1319
Qy 1390 AGTGATTACATATATGAG 1449
Db 1320 -----CAGCAGACATCTCAAGAAACAGACATCTTGTACACCTATTAACA 1362
Qy 1450 CATAAAATTTCCGAGTACAGTCTCCAGAGTTTCCACCTCGTTGTTCTCTGGATCCCTTA 1509
Db 1363 TCTGAGGTGTCAGACACCATGTTGTCAGTCTTCTCTCACTGTAGGTGAGTCAATTCAGT 1422
Qy 1510 GAACTGTGGCTGGGCTCTGTGCTTTCTGAGGAGATCCACCTTACTGAGAGAGAGAGAG 1569
Db 1423 GAAC-----AACATTTAGCAACTTCAAGAAAGCAATTCGGGC 1460
Qy 1570 AGCAGTCCATCCATGACAG 1629
Db 1461 AGAGATACCTGTGAGAGATGAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1515
Qy 1630 AAAGCAAAACCCCGGAGAGTGAATTTGTTGGTGAATCCCTGGATCCCGGAGAGTCAAGAT 1689
Db 1516 AAAGGAAATCCAGGCTGGAAATTTTCTGTTAAATCCCTTGGAGCAAAAAATGACAGAA 1575
Qy 1690 AAAATTAGAGTAAATAATTTGCTGAGCTGGGAAATGCTTGTGGGTGATGATGATGATGATG 1749
Db 1576 AAGCTCAAGGTGAAGATTTGCTGACCTTGGAAATGCTTGTGGGTGATGATGATGATGATG 1635
Qy 1750 GAAGACATCCAG 1809
Db 1636 GAAGATATTCAAACAAAGGCAATATCGTTCTTGGAGTTCTATCGGATCTGGCTATTAAT 1695
Qy 1810 ACCCTCTGGGACATCTGGAGCAGCGGTGTATGGCATTTGAGCTTGGCAACGGGAGATTAAT 1869
Db 1696 ACCCTCTGCTGACATTTGGAGCAGCGCATGATGGCTTTTGAACCTGGCCACAGGTGACTAT 1755

QY 1870 TTGTTGAACCACTTCTGGGAAGACTATTCCAGAGCGAGACACATAGCCCCACATC 1929
|||||
Db 1756 TTGTTGAACCTCATTCAGGGAAGAGTACACTCGAGATGAAGATCACATTCATTGATC 1815
|||||
QY 1930 ATAGAGCTGCTAGGCAAGTATTCGAAGGCATTTTGCTCTATCTGGAATAATATTCTCGGAA 1989
|||||
Db 1816 ATAGAATCTTCTGGGAAGTGCTCGCAAGCTCATTTGTCGAGGAAATATTCCAGGAA 1875
|||||
QY 1990 TTCTTCAATCGCAGAGAGAACTGCGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTTT 2049
|||||
Db 1876 TTTTTCACCAAAAAGGTGACCTGAAACATATCACGAAGCTGAAACCTTGGGGCCTTTT 1935
|||||
QY 2050 GATGTACTTGTGGAAGTATGCTGCGCCCATGAAGATGCTGCACAGTTTACAGATTTC 2109
|||||
Db 1936 GAGGTTCTAGTGGAAGTATGATGGTCTCAGGAAGAGCAGCTGGCTTTCAGAGATTTC 1995
|||||
QY 2110 CTGATCCGATGTTAGAAATGGTTCCAGAAACGAGCCTCAGCTGGCGAATGCCCTTCGG 2169
|||||
Db 1996 TTACTGCCCATGTTGGAGCTGATCCCTGAGAGAGAGCCACTGCCGCCGAGTGTCTCCGG 2055
|||||
QY 2170 CATCCTTGGTTGAATCTTA 2189
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Db 2056 CACCCCTTGGCTTAACCTCTA 2075
|||||

RESULT 12

US-10-172-118-875
; Sequence 875, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yundong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 875
; LENGTH: 4326
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_003137
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-875

Query Match 19.5%; Score 632.8; DB 15; Length 4326;
Best Local Similarity 60.4%; Pred. No. 3.5e-140;
Matches 1172; Conservative 0; Mismatches 672; Indels 96; Gaps 4;
QY 250 CCGAGCCAGAGAGGAGATCCTGGGATCAGATGATGAGGCAAGAGGACCTCGGGAC 309
|||||
Db 232 CAGAGCAGAGAGAGAGATCTGGGATCTGATGATGAGCAGAGATCTTAATGAT 291
|||||
QY 310 TACTGCAAGGTTGATATCATCCAGTGAATAATGGAGACCTCTTCAATGGCCGGTATCAT 369
|||||
Db 292 TATTGTAAGGAGGTTATCATCTTGTGAAAAATTTGGAGATCTATTCAATGGAGATACCAT 351
|||||
QY 370 GTATTAGAAAGCTGGAGGGGCACTTCTACTGTCTGGCTGTGGGTATGCGATGCGAG 429
|||||
Db 352 GTATCCGAAGTTAGGCTGGGACACCTTTTCAACAGATATGTTATCATGGGATATTCAG 411
|||||
QY 430 GGAAGAGATTTCTTCAATGAAGTTGTAAGAGTGCACCATTATACGGAGACAGCC 489
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Db 412 GGAAGAAATTTGTGCAATGAAAGTAGTTAAAGTGCTGAACATTACACTGAACACAGCA 471
QY 490 TTGGATGAAATAAAATTGCTCAAAATGTGTTCCAGAAAGTGTATCCAGTACGCCAAACAAA 549
|||||
Db 472 CTAGATGAAATCCGGTTGCTGAAGTCAGTTCGCAATTCAGACCCCTAATATCCAAATAGA 531
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QY 550 GACATGGTGGTCCAGCTCAATTCAGCACTTCAAGATTTTCAAGGATGAATGGATACATGTC 609
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Db 532 GAAATGGTGTTCAACTACTAGATGACTTTAAATATCAGGAGTTAATGGAACACATATC 591
|||||
QY 610 TGCATGGTCTTCCGAAGTACTTGGCCACCATCTCTCAAGTGGATCATCAAACTCAACTAT 669
|||||
Db 592 TGCATGGTATTGTAAGTTTGGGCAATCATCTGCTCAAGTGGATCATCAAACTCAATAT 651
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QY 670 CAAAGGCTCCAGTAGTGTGTGAAGAGTATCATTCGACAGTCTCTCAAGGGTTAGAT 729
|||||
Db 652 CAGGGGCTTCCATGCTGCTTGTCAAAAAAATTTATTCAGCAAGTGTGTACAGGGTCTTGAT 711
|||||
QY 730 TACTTACACAGTAAGTGAAGATCATTTACTGACATAAAGCCGAAAAATATCTTTGATG 789
|||||
Db 712 TATTTACATACCAAGTGGCGTATCATCCACTGACATTTAAACAGAGAACATCTTTATG 771
|||||
QY 790 TGTGTGGATGATGCATATGTGAGAGAATGGCAGCTGAGGCCACCTGAGTGGCAAGAAAGCA 849
|||||
Db 772 TCAGTGAATGACAGGTACATTCGAGGCTGGCTGCAGAAGCAACAGAAATGGCAGCGATCT 831
|||||
QY 850 GGTGCTCTCTCTTCCAGGCTTCCAGTGTGAGTACGGCTCCACAGCAGAAACCTATAGGA 909
|||||
Db 832 GGAGCTCTCTCCGCTTCCGATCTGCAGTCAGTACTGCTCTCCAGCTTAAACAGCTGAC 891
|||||
QY 910 AAAATATCTAAAAACAAAAGAAAAAACTGAAAAAGAAAACAGAAAGAGGAGGCTGAGTTA 969
|||||
Db 892 AAAATGTCAAAGAAATGAAGAGAAATTTGAAGAGAACAGAGCCCGGCGAGAAATTA 951
|||||
QY 970 TTGGAGAGCGCTGCGAGGAGATAGAAGAAATTTGGAGCGAGAGCTGAAAGGAAAAATA 1029
|||||
Db 952 CTAGAGAGCGAATGCAGAAATTTAGGAAATTTGAGAAAGAGTCCG----- 997
|||||
QY 1030 GAAGAAACATCACCTCAGCTGCACCTTCCAATGACCAGATGGCGAAATCTGCCCCAGAG 1089
|||||
Db 998 -----GCCCTTGGGCAAAAAGACCAAAAC 1020
|||||
QY 1090 GTGAAACTAAAAACAACAGGATTTAGAGGAGCGGCTGAGCGCAGAGACTGCAAAAGGACAAT 1149
|||||
Db 1021 AAGCAAGAGAAATCAGAGTCTCTGTTGAAGACCTTTGAAAGAGAACCCACCTAATAAA 1080
|||||
QY 1150 GGTGAAGCTGAGGACCCAGGAGAGAAAGAGATGCTGAGAAAGAAAAACATTTGAAAAAGAT 1209
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Db 1081 ATGACCCAGAAAAACTTGAAGAGTCAAGTACCATTGGCCAGGATCAACGCTTATGGAA 1140
|||||
QY 1210 GAAGATGATGTAGATCAGGAACCTTGGGAACATAGACCTTACGTGGATAGAATCACCTAAA 1269
|||||
Db 1141 CGTGATACAGAGGGTGTGCGACAGAAATTAATTTGCAATGGAGTGTGTTGAAGTCATTAAT 1200
|||||
QY 1270 ACCAATGGCCATATTGAGAAATGGCCCATTTCTCAGTGGAGCAGCACTGGACGATGAAGAT 1329
|||||
Db 1201 TATATCTCAGAACAGTAATAATAAGAACTTGAGACATAAAGAGGATCTACATAATGCTAAT 1260
|||||
QY 1330 GATGATGAAGAAAGACTGCCCCAAATCCTGAGGAATAATAATCTTGATGAGCCAAATGCAGAA 1389
|||||
Db 1261 GACTGTGATGTCCAAAATTTGAATCAGGAATCTAGTTTCTTAAGTCTCCCAATGGAGA- 1319
|||||
QY 1390 AGTGATTACATATATAGACGCTCTTATGAACAAATTCATGGTGAATTTGCCAAATGGACGA 1449
|||||
Db 1320 -----CAGCAGCACATCTCAAGAAAACAGACTCTTTGTACACCTATAACA 1362
|||||
QY 1450 CATAAAATTCGAGTGCACAGTTCCAGAGTTTCCACCTCGTTGTTCTCTCGATCCTTA 1509
|||||
Db 1363 TCTAGGTTGTACAGACCAATGTTGTGCCAGTCTTCTCTCAACTGTAGGTGAGTCAITTCAGT 1422
|||||
QY 1510 GAACTGTGGCTGGGCTCTGTGCTTTCTGAGGGATCACCACTTACTGCAAGAGGAG 1569
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Db 1423 GAAC-----AACACATTACGCAACTTCAAGAAAGCATTCGGGC 1460
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; ORGANISM: Homo sapiens		Query Match		19.5%; Score 632.8; DB 16; Length 4326;	
US-10-342-887-875		Best Local Similarity		60.4%; Pred. No. 3.5e-140;	
		Matches 1172; Conservative		0; Mismatches 672; Indels 96; Gaps 4;	
QY	1570	AGCAGTCCATCCATGACAGAGAGAAACGGTTTCAGCCTCAGTACTGCGGATTTGCCA	1629		
DB	1461	AGAGATACCTGTGAAGATGAACAGAGCAAGAACATAACGACCACTGGACAC-----AC	1515		
QY	1630	AAAGCAAAACCCGGCAGCTGACTTGTGTGTAATCCCTGGATCCCGGAATGCAGAT	1689		
DB	1516	AAAGGAAATCCACGGCTGGAAATTTCTTGTTAATCCCTTGAGCCAAATAATGCAGAA	1575		
QY	1690	AAAAATTAGAGTAAAAAATGCTGACCTGGGAAATGCTTGTGGGTGCATAAACCTCAAG	1749		
DB	1576	AGCTCAAGTGAAGATTGCTGACCTTGGAATGCTTGGGTGCACAAACATTTCACT	1635		
QY	1750	GAAGACATCCAGCGCTCAGTACCGCTCCATAGAGTTTAAATAGGAGCGGGTACAGC	1809		
DB	1636	GAAGATATTCAACCAAGGCAATATCGTTCTTGGAAAGTTCTAATCGGATCTGGCTATAAT	1695		
QY	1810	ACCCCTGGGACATCTGGAGCAGCGGTGTATGCAATTTGAGCTGGCAACGGGAGATTAT	1869		
DB	1696	ACCCCTGGTGACATTTGGAGCACGGCATGCGATGGCTTTGAACTGGCCACAGGTGACTAT	1755		
QY	1870	TTGTTTGAACCACTTCTGGGAAAGACTATTCCAGAGAGAAACCAATAGCCCAATC	1929		
DB	1756	TTGTTTGAACCTCAITTCAGGGGAAGAGTACACTCGAGATGAAGATCACATTTGATGATC	1815		
QY	1930	ATAGAGCTCTAGGAGTATTCAGAGGCACTTTGCTCTATCTGGAAATATTCTCGGAA	1989		
DB	1816	ATAGAACTTCTGGGGAAGTGCTCGCAAGCTCAITTTGGCAGGAAATATTCCAAGGAA	1875		
QY	1990	TTCTTCAATCGCAGAGGAAACTTGCACACATCACCAAGCTGAAAGCCCTGGAGCCTCTTT	2049		
DB	1876	TTTTTCAACAAAAGGTGACCTGAAACATATACGAAGCTGAAACCTTTGGGGCCTTTT	1935		
QY	2050	GATGTACTTGTGGAAAGTATGGCTGGCCCATGAAGATGCTGCACAGTTTACAGATTTC	2109		
DB	1936	GAGGTTCTAGTGAGAAGTATGAGTGGTCTCGAGGAGAGCGCAGCTGGCTTTCACAGATTTC	1995		
QY	2110	CTGATCCGATGTTAGAAATGGTTCCAGAAACAGAGCCTCAGCTGGCGAATGCCCTTCGG	2169		
DB	1996	TTACTGCCCATGTTGAGCTGATCCCTGAGAGAGACCACTGCCCGCAGTGTCTCCGG	2055		
QY	2170	CATCCTTGGTTGAATCTTTA 2189			
DB	2056	CACCTTGGCTTAACCTTA 2075			
RESULT 13					
US-10-342-887-875					
; Sequence 875, Application US/10342887					
; Publication No. US20040058340A1					
; GENERAL INFORMATION:					
; APPLICANT: Dai, Hongyue					
; APPLICANT: He, Yudong					
; APPLICANT: Linsley, Peter S.					
; APPLICANT: Mao, Mao					
; APPLICANT: Roberts, Christopher J.					
; APPLICANT: Van 't Veer, Laura Johanna					
; APPLICANT: Van de Vijver, Marc J.					
; APPLICANT: Bernards, Rene					
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients					
; FILE REFERENCE: 9301-188-999					
; CURRENT APPLICATION NUMBER: US/10/342.887					
; PRIOR FILING DATE: 2003-01-15					
; PRIOR APPLICATION NUMBER: 60/298,918					
; PRIOR FILING DATE: 2001-06-18					
; PRIOR APPLICATION NUMBER: 60/380,710					
; PRIOR FILING DATE: 2002-05-14					
; PRIOR APPLICATION NUMBER: 10/172,118					
; PRIOR FILING DATE: 2002-06-14					
; NUMBER OF SEQ ID NOS: 2699					
; SEQ ID NO 875					
; LENGTH: 4326					
; TYPE: DNA					

Db 1141 CGGTATACAGAGGGTGGTGCAGCAGAAATTAATTTGCAATGGAGTGAATGAAATCAATTAAT 1200
Qy 1270 ACCAATGGCCATATTCAGAAATGCCCCATCTCTCTGAGCAGCAAGCACTGACGATGAAGAT 1329
Db 1201 TATACACAGACAGTAAATGAACATTAAGACATTAAGAGAGGATCTACATATGTAAT 1260
Qy 1330 GATGATGAAGAGACAGTCCCAATCTCTGAGGAATATAATCTTGATGAGCAATGAGCA 1389
Db 1261 GACTGTGATGTCAAAATTTGAATCAGGAATCTAGTTTCTTAAGTCTCCAAATGAGAA- 1319
Qy 1390 AGTGATATACATATAGCAGCTCTATGAACAATTCATGAGTGAATTCGCAATGAGCA 1449
Db 1320 -----CAGCAGCAGATCTCAAGAAACAGACTCTTGACACCTATAACA 1362
Qy 1450 CATATAATTCAGAGTACAGTTCCAGAGATTTTCCACCTCGTTGTTCTCTGATGATCCTTA 1509
Db 1363 TCTGAGGTGTCAGACACCATGTTGTCAGTCTTCTCACTGAGTCTTCTCACTGAGTCAATCA 1422
Qy 1510 GAACCTGTGGCCTGCGGCTCTGTGCTTCTGAGGATCACTTACTGAGCAAGAGGAG 1569
Db 1423 GAAC-----AACATTAGCCAACTTCAAGAAAGCAATTCGGGC 1460
Qy 1570 AGCAGTCCATCCCATGACAGAGCAGAGCGTTTTCAGCCCTCCAGTACTGCGGATTTGCCA 1629
Db 1461 AGAGATACCTGTGAAGATGAACAAGCAAGCAATACGAGCACTGGACA-----AC 1515
Qy 1630 AAGCAAAAACCGGCGAGTCACTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1689
Db 1516 AAGGAAAAATCCACGCTGGAATTTTCTTTGTTAAATCCCTTTGAGCCAAAATGAGAA 1575
Qy 1690 AAAATTTAGATGAAAAATCTGACCTGGGAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1749
Db 1576 AAGCTCAAGGTGAAGATGCTGACCTTGGAAATGCTTGTGGTGGTGGTGGTGGTGGTGGTGGT 1635
Qy 1750 GAAGACATCCAGACCGGTGAGTACCGCTCCATAGAGTTTAAATAGGAGCGGGTACAGC 1809
Db 1636 GAAGATATTCAAACAGGCAATATCGTTCTTGGAAATTCATCGATCTGGCTATAT 1695
Qy 1810 ACCCTGCGGACATCTGGAGCAGCGGTGATGGCAATTTGAGCTGGCAACGGGAGATAT 1869
Db 1696 ACCCTGCTGACATTTGGAGCAGCGCATGCGGCTTTGAACTGGCCACAGGTGACTAT 1755
Qy 1870 TTGTTGAACCACTCTCGGGAAGACTATTCAGAGAGCAGAGACACACATAGCCACATC 1929
Db 1756 TTGTTGAACCTCATTCAGGGGAAGAGTACCTCGAGATGAAGATCACATTCGATTTGATC 1815
Qy 1930 ATAGAGCTGCTAGGCAAGTATTCAGGCACTTTGCTCTATCTGAAAAATATTCCTCGGAA 1989
Db 1816 ATAGAACTTCTGGGAGGTGCTTCAGACTCATTTGTCGAGCAAAATATTCAGAGGA 1875
Qy 1990 TTCTTCAATCGCAGAGAGAACTGCGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTT 2049
Db 1876 TTTTTCACAAAAGGTGACCTGAAACATATCACGAAGCTGAACCTTTGGGCGCTTTT 1935
Qy 2050 GATGATCTTGTGAAAAGTATGCTGGCCCCATGAAGATGCTGCAAGTTTACAGATTTTC 2109
Db 1936 GAGGTTCATAGTGAGAGATGATGAGTGGTCTCAGGAAGAGGCACTGGCTTTCAGATTTTC 1995
Qy 2110 CTGATCCGATGTTAGAAATGGTTCCAGAAAAACGAGCCTCAGCTGGCGAATGCTTCGG 2169
Db 1996 TTACTGCCATGTTGAGCTGATCCCTGAGAGAGAGCCACTGCGCCCGAGTGTCTCCGG 2055
Qy 2170 CATCTTGGTTGAATTTCTTA 2189
Db 2056 CACCCTTGGCTTAACCTCTTA 2075

RESULT 14

US-10-252-157-374
; Sequence 374, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
; APPLICANT: Paris, Mary

; APPLICANT: Pearson, Cecelia I.
; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: PA-0027-1 US
; CURRENT APPLICATION NUMBER: US/10/252,157
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,048
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: PERL Program
; SEQ ID NO 374
; LENGTH: 4349
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030190640A1 474724.5
US-10-252-157-374

Query Match 19.4%; Score 629.6; DB 15; Length 4349;
Best Local Similarity 60.3%; Pred. No. 2.1e-139;
Matches 1170; Conservative 0; Mismatches 674; Indels 96; Gaps 4;
Qy 250 CCGGAGCCAGAGAGGAGATCTTGGGATCAGATGATGAGGAGCAAGGAGCCCTGGGAC 309
Db 232 CCAGAGCAGAGAGAGGATCTTGGGATCTGATGATGAGCAAGAGATCTTAATGAT 291
Qy 310 TACTGCAAAAGGTGGATATCATCCAGTGAATAATGGAGACCTCTTCAATGGCCGGTATCAT 369
Db 292 TATTGTAAAGAGGTATCATCTTGTGAAAAATTTGGAGATCTATTCAATGGAGATACCAT 351
Qy 370 GTTATTAGAAAGCTTGGATGGGGGACCTTCTACTGTCTGCTGTGCTGGGATATGCGAG 429
Db 352 GTGATCCGAAAGTTAGGCTGGGGACACTTTTCAACAGATATGTTATCATGGGATATTCAG 411
Qy 430 GCGAAAAAGATTTTGTGCAATGAAAGTTGTAAAAAGTGCACGATTTATACGGAGACAGCC 489
Db 412 GGGAGAAATTTTGTGCAATGAAAGTTGTAAAAAGTGTGAACATTTACACTGAAACAGCA 471
Qy 490 TTGGATGAAATAAAAATTTGCTCAAAATGTGTTGAGAAAGTGTATCCAGTACCCCAACAAA 549
Db 472 CTAGATGAAATCCGGTTGCTGAAGTCAGTTGCAATTCAGACCCCTAATATCCAAATAGA 531
Qy 550 GACATGGTGGTCCAGCTCATTTGACGACTTCAAGATTTTCAAGGATGATGGGATACATGTC 609
Db 532 GAAATGGTGTTCACACTACTAGTGAATTTTAAATATCAGGAGTTAATGGAACACATATC 591
Qy 610 TGCATGGTCTTCCAGATGACTTGGCCACCATCTCTCAAGTGGATCATCAATCCAACTAT 669
Db 592 TGCATGGTATTTGAAGTTTGGGGCATCATCTGCTCAAGTGGATCATCAATCCAACTAT 651
Qy 670 CAAGGCTCCCAAGTACGTTGTGTAAGAGTATCATTTGCAAGTCCCTTCAAGGGTTAGAT 729
Db 652 CAGGGCTTCCACTGCTTGTGTCAAAAAATTTATTCAGCAAGTGTTCACAGGCTTGTAT 711
Qy 730 TACTTACAGATGAAGTGAAGATCATTTACTATGACATTAAGCCGGAATAATCTTTGATG 789
Db 712 TATTTACATACCAAGTGGCGGTATCATCCACATGACATTTAAACCCAGAGAACATCTTTAT 771
Qy 790 TGTGTGGATGATGATATGTTGAGAGAAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCA 849
Db 772 TCAGTGAATGACAGTACATTCGGAGGCTGGCTGCAAGAGCAACAGATGGCAGCGATCT 831
Qy 850 GGTGCTCTCTCTCTTTCAGGGTCTGAGTGAAGTACGGCTCCACAGAGAAACCTATAGGA 909
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Qy 970 TTGGAGAGCGCTGCGAGGAGATAGAAGAAATTTGGAGCGAGAGCTCTGAAAGGAAAAATA 1029
Db 952 CTAGAGAGCGAATGCGGAAATTTGAGGAAATTTGAGAAATGAGAAAGAGTCTCG----- 997

QY 1030 GAAGAAAACATCACCTCAGCTGCACCTTCCATGATGACAGGATGGCGAATATCTGCCAGAG 1089
 Db 998 -----GCCCTGGGCAAAAAGAACCAAC 1020
 QY 1090 GTGAAGAACTAAACCAACAGGATTAGAGGAGGGCTGAGGCGAGAGACTGCAAGAGCAAT 1149
 Db 1021 AAGCAGAGAAATCAGAGAGTCTCTGTTGAAGACCTTGAAGAGAGAGAGAGAGAGAGAGAG 1080
 QY 1150 GGTGAAGCTGAGGACGACGAG 1209
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 QY 1210 GAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1269
 Db 1141 CGTGATACAGAGGGTGGTGCAGAGAGAAATTAATGCAATGGAGTGAATGAAGTCAATTAAT 1200
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 Db 1201 TATACTCAGACNGTAAATGAACATTTGAGACATGAAGAGAGATCTACATAATGCTAAT 1260
 QY 1330 GATGATGAAGAGACTGCCCAATCTCTGAGGATATAATCTTGATGAGCCCAATGCAGAA 1389
 Db 1261 GACTGTGATGTCAAAATTTGAATCAGGAATCTAGTTTCTTAAGCTCCCAAAATGGAGA- 1319
 QY 1390 AGTGATTACATATAGCAGCTCTATGAACAATTCATGGTGAATTTGCAAAATGGACGA 1449
 Db 1320 -----CAGCAGCAGATCTCAAGAAACAGACTTGTGACACCTATNACA 1362
 QY 1450 CATAAAATCCCGAGTACAGATTTCCAGAGATTTCCACCTGTTGTTCTCTGGATCCTTA 1509
 Db 1363 TCTGAGTGTGACAGACCATGGTGTGCGAGTCTTCTCACTGATGAGTCAATTCAGT 1422
 QY 1510 GAACCTGTGCGCTGGCTCTGTGCTTTCTGAGGATCACCATTACTGAGCAAGAGGAG 1569
 Db 1423 GAAC-----AACACATTAGCCAACTTCAAGAAAGCATTTCCGGC 1460
 QY 1570 AGCAGTCCATCCATGACAG 1629
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 QY 1930 ATAGAGTGTGAGGAGTATTCAGGCACTTTGCTCTATCTGATGAATATTTCTCGGAA 1989
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 QY 2050 GATGTACTTGTGGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2109
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 Db 2056 CACCTTGGCTTAACCTCTA 2075
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 ; Sequence 21987, Application US/09814353
 ; Publication No. US20030165831A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lee, John
 ; APPLICANT: Thompson, Pamela
 ; APPLICANT: Lillie, James
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
 ; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
 ; FILE REFERENCE: MRI-006B
 ; CURRENT APPLICATION NUMBER: US/09/814,353
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: US 60/191,031
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: US 60/207,124
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: US 60/211,940
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: US 60/216,820
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/220,661
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/257,672
 ; PRIOR FILING DATE: 2000-12-21
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 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 21987
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 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 4427, 4428, 4429, 4430, 4431, 4432, 4433, 4434, 4435, 4436,
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 ; LOCATION: 4447, 4448, 4449, 4450, 4451, 4452, 4453, 4454, 4455, 4456,
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 ; OTHER INFORMATION: n = A,T,C or G
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 QY 490 TTGATGAAATTAATTAATTTGCTCAATGCTGTTCCAGAAAGAGTCCAGTCCAGCAACAA 549
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Qy	610	TGCATGCTCTTCAAGTACTTGGCCACCATCTCTCAAGTGGATCATCAAAATCCAACAT	669
Db	580	TGCATGGTATTTGAAGTTTTGGGCACTCACTGCTCAAGTGGATCATCAAAATCCAATAT	639
Qy	670	CAAGGCTCCCAAGTACGTTGTGTGAAGAGTATCAATCGACAGGTCCTTCAAGGGTTAGAT	729
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Qy	730	TACTTACACAGTAAAGTCAAGATCAATTCATACATTAAGCCGGAAAAATATCTTGAATG	789
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Qy	850	GGTGCTCCTCTCTTCCAGGCTGTGACGTAGTACGGCTCCACAGCAGAAACCTATAGGA	909
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Qy	910	AAAATATCTAAATAACAAAGAAAAAACTGAAAAGAAAACAGAAGAGCGAGCTGAGTTA	969
Db	880	AAAATGTCAAGAATAAAGAAGAAATAATGAAGAAGAAAGCAGAGCCCGAGCAGAAATTA	939
Qy	970	TTGAGAAGCGCCTGCAAGGAGATAGAAGAAATTTGAGCGAGAAGCTGAAAAGAAAAATAA	1029
Db	940	CTAGAGAAGCGAATGCAAGAAATTTGAGAAATGGAAGAAAGTCCG	985
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Db	1069	ATGACCACAAAGAAAACCTTGAAGAGTCAAGTACCATTGCGCCAGGATCAACCGCTTATGAA	1128
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Qy	1750	GAAGACATCCAGACGCGCTCAGTACCGCTCCATAGAGGTTTTTAATPAGGAGCGGGTACAGC	1809
Db	1624	GAAGATATCAAACAAGCAATATCGTTCTTGAAGTTCTAATCGATCTGGCTATAAT	1683
Qy	1810	ACCCCTGGGACATCTGGAGACGGCGTGTATGGCATTTGAGCTGGCAACGGGAGATTAT	1869
Db	1684	ACCCCTGCTGACATTTGGAGCAGCGCATGATGGCCTTTGAACTGGGCCACAGGTGACTAT	1743
Qy	1870	TTGTTTGAACCAATCTGGGGAGACTATTTCCAGAGACCAAGACCAATAGCCCATC	1929
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Qy	1930	ATAGAGCTGTGGGACGATATTTCAAAGGCACTTTTGCTCTATCTGGAATAATTTCTCGGGAA	1989
Db	1804	ATAGAACTTTGGGGAAGGTGCCTCGCAAGCTCATTTGTGCGAGGAATATTTCCAGGAA	1863
Qy	1990	TTCTTCAATCGCAGAGAGAACTGCGACATCAACCAAGCTGAAGCCCTCGAGCCTCTTT	2049
Db	1864	TTTTTCCAAAAAAGGTGACCTGAAACATATCACGAAGCTGAAACCTTTGGGGCCTTTTT	1923
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Qy	2110	CTGATCCCGATGTTAGAAAAATGGTTCCAGAAAAACGAGCCCTCAGCTGGCGGAATGCCTTCGG	2169
Db	1984	TTACTGCCCATTTGTGAGCTGTATCCCTTGAGAAGAGAGCCACTGCGCCCGAGTGTCTCCGG	2043
Qy	2170	CATCCTTGGTGAATTTCTTA	2189
Db	2044	CACCTTGGCTTAACTCTTA	2063

Search completed: January 23, 2005, 23:48:08
Job time : 1675.02 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 23, 2005, 05:33:48 : Search time 254.768 Seconds
(without alignments)
9075.705 Million cell updates/sec

Title: US-10-799-676-1
Perfect score: 3253
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2595.6	79.8	2791	2	US-09-016-000-8
4	666.2	20.5	90541	4	US-09-759-359A-3
5	666.2	20.5	90541	4	US-10-207-973-3
6	632.8	19.5	4299	1	US-08-264-002-1
7	629.4	19.3	923	4	US-09-016-434-703
8	293.4	9.0	1427	3	US-09-173-581-10
9	293.4	9.0	1427	3	US-09-420-915-10
10	254	7.8	793	4	US-09-016-434-79
11	248	7.6	249	4	US-09-016-434-808
12	177.2	5.4	617	3	US-09-385-982-396
13	162.4	5.0	2100	1	US-08-264-002-6
14	159.2	4.9	1731	4	US-09-248-796A-6406
15	117	3.6	569	4	US-09-270-767-1008
16	117	3.6	569	4	US-09-270-767-16290
17	99.6	3.1	7218	1	US-08-232-463-14
18	97.6	3.0	326	4	US-09-513-999C-10592
19	92.8	2.9	641	4	US-09-270-767-1313
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21	62.6	1.9	891	4	US-09-248-796A-11247
22	60.6	1.9	51259	3	US-08-781-891-209
23	60.6	1.9	51259	4	US-09-618-166-209
24	59.8	1.8	1669	3	US-09-461-697-184
25	59.2	1.8	696	3	US-09-461-697-193
26	59.2	1.8	699	3	US-09-461-697-191
27	59.2	1.8	717	3	US-09-461-697-189

28	59.2	1.8	774	3	US-09-461-697-187	Sequence 187, App
29	59.2	1.8	819	3	US-09-461-697-185	Sequence 185, App
30	57.6	1.8	3211	2	US-08-574-959A-8	Sequence 8, Appli
31	57.6	1.8	3211	3	US-09-357-014-8	Sequence 8, Appli
32	57.6	1.8	3901	2	US-08-574-959A-6	Sequence 6, Appli
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34	57	1.8	1141	4	US-09-806-708B-22	Sequence 22, Appli
35	55.8	1.7	1434	4	US-09-248-796A-5873	Sequence 5873, Ap
36	55.8	1.7	2409	4	US-09-614-221A-204	Sequence 204, App
37	55.8	1.7	3095	6	5231168-1	Patent No. 5231168
38	55.4	1.7	699	4	US-09-248-796A-9722	Sequence 9722, Ap
39	55.4	1.7	7218	1	US-08-232-463-14	Sequence 14, Appli
40	55	1.7	832	4	US-09-621-976-2813	Sequence 2813, Ap
41	55	1.7	1737	4	US-09-248-796A-581	Sequence 681, App
42	54.8	1.7	478	4	US-09-621-976-10407	Sequence 10407, A
43	54.8	1.7	2223	1	US-08-257-073-4	Sequence 4, Appli
44	54.2	1.7	3337	1	US-08-072-610-1	Sequence 1, Appli
45	54.2	1.7	3337	2	US-08-719-822B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09759359A
; Patent No. 6492153
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEROF
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/09/759,359A
; CURRENT FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3253
; TYPE: DNA
; ORGANISM: Human
US-09-759-359A-1

Query Match	100.0%	Score 3253;	DB 4;	Length 3253;
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Matches 3253;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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Db	61	AGCCCCCGCCCGCTTCGCGCGCTCGGAATGAGCTCCCGGAAAGTGTGGCCATTTCAG	120	
QY	121	GCCGAAAGCGAGGCGGAAAGAGAGAAACATCCGAAAGCGCGAGGCTCAACAGAAA	180	
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QY	181	GCTCTTTAGTTCTCTCTCCCGCCACACACACACACACACACCTTTGCCAGAC	240	
Db	181	GCTCTTTAGTTCTCTCTCCCGCCACACACACACACACACACCTTTGCCAGAC	240	
QY	241	CCACACACCCCGGAGGAGGAGGATCCTGGGATCAGATGATGAGGAGCAAGAGGAC	300	
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QY	301	CTGCGGACTACTGCAAAAGGTGGATATCATCCAGTGAATAATGGAGACCTCTTCAATGGC	360	
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QY	361	CGGTATCATGTTATTAGAAAGCTTGATGGGGGCACTTCTCTACTCTCTGGCTGCTGG	420	

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1261	TCACCTAAAAACCAATGGCCATATTGAGAAATGGCCCATTTCTCAGTGGAGCAGCACTGGAC	1320
1321	GATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1380
1321	GATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1380
1381	AATGCAGAAAGTGATTAACACATATAGCAGCTCCTATGAACAAATTCATTTGGTGAATGCCA	1440
1381	AATGCAGAAAGTGATTAACACATATAGCAGCTCCTATGAACAAATTCATTTGGTGAATGCCA	1440
1441	AATGACGACATAAAATTTCCGAGTTCACAGTTCACAGATTTTCCACTCGTTGTTCTCT	1500
1441	AATGACGACATAAAATTTCCGAGTTCACAGTTCACAGATTTTCCACTCGTTGTTCTCT	1500

QY	1501	GGATTCCTTAGAACCTGTGTGCCCTGCGGCTCTGTGCTTCTGAGGGATCACCACCTTACTCTGAG	1560
DB	1501	GGATTCCTTAGAACCTGTGTGCCCTGCGGCTCTGTGCTTCTGAGGGATCACCACCTTACTCTGAG	1560
QY	1561	CAGAAGAGAGCAGTCCATCCATCAGACAGAAAGCAGACGGTTCCTCAGCTCCAGTACTGGG	1620
DB	1561	CAGAAGAGAGCAGTCCATCCATCAGACAGAGCAGACGGTTCCTCAGCTCCAGTACTGGG	1620
QY	1621	GAATTCGCAAAAGCAAAAACCCGGGGCAGCTGACTTGTGTGGTGAATCCCTTGGATCCCGGG	1680
DB	1621	GAATTCGCAAAAGCAAAAACCCGGGGCAGCTGACTTGTGTGGTGAATCCCTTGGATCCCGGG	1680
QY	1681	AATGCAGATAAATTAGTGTAATAAATTCGTGACCTGGGAAATGCTTGTGTGGTGCATAAAA	1740
DB	1681	AATGCAGATAAATTAGTGTAATAAATTCGTGACCTGGGAAATGCTTGTGTGGTGCATAAAA	1740
QY	1741	CACCTTCACGGAAGACATCCAGACGGGTCAAGTACCGCTCCATAGAGGTTTTAATAGGAGCG	1800
DB	1741	CACCTTCACGGAAGACATCCAGACGGGTCAAGTACCGCTCCATAGAGGTTTTAATAGGAGCG	1800
QY	1801	GGGTACAGCACCCCTGGGACATCTGGAGCAGCGCGTGTATGGCATTTGACCTGGCACAACG	1860
DB	1801	GGGTACAGCACCCCTGGGACATCTGGAGCAGCGCGTGTATGGCATTTGACCTGGCACAACG	1860
QY	1861	GGCAGTATTATTGTTTGAACCAACATCTCGGGGAAGACTATTCACAGAGACGAAGCCACATA	1920
DB	1861	GGCAGTATTATTGTTTGAACCAACATCTCGGGGAAGACTATTCACAGAGACGAAGCCACATA	1920
QY	1921	GCCACATCATAGAGCTGCTGAGCAGTATTCACAGGCATTTGCTCTATCTCGGAATAAT	1980
DB	1921	GCCACATCATAGAGCTGCTGAGCAGTATTCACAGGCATTTGCTCTATCTCGGAATAAT	1980
QY	1981	TCTCGGGAATCTTCAATCCAGAGAGAACTGCACACATCACCAAGCTGAAGCCCTGG	2040
DB	1981	TCTCGGGAATCTTCAATCCAGAGAGAACTGCACACATCACCAAGCTGAAGCCCTGG	2040
QY	2041	AGCCTCTTTTGATGTACTTGTGGAAAAAGTATGGCTGCGCCCATGAAAGATGCTGCACAGTTT	2100
DB	2041	AGCCTCTTTTGATGTACTTGTGGAAAAAGTATGGCTGCGCCCATGAAAGATGCTGCACAGTTT	2100
QY	2101	ACAGATTCCTGATCCCGATGTTAGAAATGGTTCCAGAAAAACGAGCCCTCAGCTGGCGAA	2160
DB	2101	ACAGATTCCTGATCCCGATGTTAGAAATGGTTCCAGAAAAACGAGCCCTCAGCTGGCGAA	2160
QY	2161	TGCGCTTCGGCATCCTTGTTGAAATCTTAGCAAAATCTACCAATATGCAATTCAGCTA	2220
DB	2161	TGCGCTTCGGCATCCTTGTTGAAATCTTAGCAAAATCTACCAATATGCAATTCAGCTA	2220
QY	2221	GCAAAATGTTCCAGTACATTTGGACCTTAAACGGGTGACTCTCATTCCTTTAAACAGGATACAA	2280
DB	2221	GCAAAATGTTCCAGTACATTTGGACCTTAAACGGGTGACTCTCATTCCTTTAAACAGGATACAA	2280
QY	2281	GTGAGCTGGCTTCATCTCCTCAGACCTTTATTTTGTCTTTGAGTACTGTTGTTGACATTTT	2340
DB	2281	GTGAGCTGGCTTCATCTCCTCAGACCTTTATTTTGTCTTTGAGTACTGTTGTTGACATTTT	2340
QY	2341	GCTTTTGTGCACTGTGATCTGGGAAAGGGTAGTCTTTTGTCTTCAGCTTAAGTAGTTTA	2400
DB	2341	GCTTTTGTGCACTGTGATCTGGGAAAGGGTAGTCTTTTGTCTTCAGCTTAAGTAGTTTA	2400
QY	2401	CTGACCATTTTCTCTGGAAACAATAACATGCTCTCTAAGCATTTGTTTCTGTGTTCTGTG	2460
DB	2401	CTGACCATTTTCTCTGGAAACAATAACATGCTCTCTAAGCATTTGTTTCTGTGTTCTGTG	2460
QY	2461	ACATTCCAAATGTCATTTTTTTTGAATGAAAAATACTTTTCCCTTGTGTTTTTGGCAGGTTT	2520
DB	2461	ACATTCCAAATGTCATTTTTTTTGAATGAAAAATACTTTTCCCTTGTGTTTTTGGCAGGTTT	2520
QY	2521	TGTAACTATTTATGAAGAAATAATTTAGCTCAGTACTATATAATTTACAATCTTAAGAAA	2580
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Db 1081 TGCCAGAGGTGAATCTAAAACAACAGATTAGAGGAGCGGTGAGGCAGAGCTGCA 1140
Qy 1141 AAGGCAATGTGTGAAGCTGAGGACAGAGGAGAAAGAGATGCTGAGAAAGAAAACATT 1200
Db 1141 AAGGCAATGTGTGAAGCTGAGGACAGAGGAGAAAGAGATGCTGAGAAAGAAAACATT 1200
Qy 1201 GAAAAGATGAAGATGATGATAGATCAGGAACTTGGGAACATAGACCCCTACCTGATAGAA 1260
Db 1201 GAAAAGATGAAGATGATGATAGATCAGGAACTTGGGAACATAGACCCCTACCTGATAGAA 1260
Qy 1261 TCACCTTAAACCAATGGCCATATTGAGAAATGGCCCAATTCTCACTGGAGCAGCAACTGGAC 1320
Db 1261 TCACCTTAAACCAATGGCCATATTGAGAAATGGCCCAATTCTCACTGGAGCAGCAACTGGAC 1320
Qy 1321 GATGAAGATGATGATGAAGAAGCTGCCCCAAATCTCTGAGGAATATAAATCTTGTGAGCCA 1380
Db 1321 GATGAAGATGATGATGAAGAAGCTGCCCCAAATCTCTGAGGAATATAAATCTTGTGAGCCA 1380
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Qy 1441 AATGCAGCAATAAAATCTCCGAGTACACAGATTTCCAGAGATTTCCACCTCGTTGTTCTCT 1500
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Db 1501 GATCCTTGAACCTGTGGCTCGGGCTCTGCTGCTTCTGAGGGATCACCATTACTGAG 1560
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Db 1621 GATTTGCCAAAAGCAAAAACCCGGGACAGTCTGTTGGTGAATCCCTCGATCCGGGG 1680
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Db 1741 CACTTCACGGAAGACATCCAGACGCTCAGTACCGCTCCATAGAGGTTTTTAATAGAGCG 1800
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Db 1801 GGGTACAGCACCCCTGCGGACATCTGGAGCACGGCGTGTATGGCATTTGAGCTGGCAACG 1860
Qy 1861 GGAGATTATTTGTTGAAACACATCTGGGGAAGACTATTCCAGAGACGAAACACACATA 1920
Db 1861 GGAGATTATTTGTTGAAACACATCTGGGGAAGACTATTCCAGAGACGAAACACACATA 1920
Qy 1921 GCCCACATCATAGAGCTGCTAGGAGTATTCCAGGCACTTTGCTCTATCTGGAATAAT 1980
Db 1921 GCCCACATCATAGAGCTGCTAGGAGTATTCCAGGCACTTTGCTCTATCTGGAATAAT 1980
Qy 1981 TCTCGGAATTTCTTCAATCGCAGAGGAGAACTGGCAACATCCAGCTGGAAGCCCTGG 2040
Db 1981 TCTCGGAATTTCTTCAATCGCAGAGGAGAACTGGCAACATCCAGCTGGAAGCCCTGG 2040
Qy 2041 AGCCTCTTGTATGATGTTGTTGAAAAGTATGGCTGGCCCATGAAGATGCTGCACAGTTT 2100
Db 2041 AGCCTCTTGTATGATGTTGTTGAAAAGTATGGCTGGCCCATGAAGATGCTGCACAGTTT 2100
Qy 2101 ACAGATTTCTGATCCCGATTTAGAAAATGTTTCCAGAAAAACAGGCTCAGCTGGCGAA 2160
Db 2101 ACAGATTTCTGATCCCGATTTAGAAAATGTTTCCAGAAAAACAGGCTCAGCTGGCGAA 2160
Qy 2161 TGCCTTGGCATCTCTGGTGAATCTTAGCAAAATCTTACCAATATTGCAATTTCTGAGCTA 2220

Db 2161 TGCTTTGGCATCTCTGGTGAATCTTAGCAAAATCTTACCAATATTGCAATCTGAGCTA 2220
Qy 2221 GCAAAATGTTCCAGTACATTGGACCTAAAACGGTGAATCTCTCATTTCTTTAAACAGGATTACAA 2280
Db 2221 GCAAAATGTTCCAGTACATTGGACCTAAAACGGTGAATCTCTCATTTCTTTAAACAGGATTACAA 2280
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Db 2281 GTGAGCTGGCTTCATCCTCAGACCTTTATTTCTGCTTTGAGGTACTGTTGTTGACATTTT 2340
Qy 2341 GCTTTTGTGACATGTCATCTCGGGAAGGTAAGTCTTTTGTCTTCTCAGCTTAAGTAGTTTA 2400
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Db 2401 CTGACCAATTTCTTTCTGGAACCAATAACATGTCTCTAAGCAATTTGTTTGTGTGTGTG 2460
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Db 2581 TTATCAAGTTGGGAAACCAAGAAATAGCAAGGGAATGTACAATTTTATCTCTCGGCAAA 2640
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Db 2641 GGGACATCTCTGTTATTTATAGTATGTAATGACACCTGTAAATGTTTACTTTGATTT 2700
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Db 2821 ATTAATACTACTTAATAATACCTTTCTTTGTTTTTTGTTTTTCTTATTTTCAATTT 2880
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Db 2881 AAAATCAATAATCAAAAACCCCACTATAGTCCAACGACAAATTCATTTCTGGCGGTCAACTT 2940
Qy 2941 TTTTAACTCTTATAGTACTGAGACTCTGGTGTCTCAATATTAATATTTCTAAATCTAC 3000
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Db 3001 CACCAAGTTAGCCCGTAATGTCTCTCTCGTGAATCTGTCATACATAATTTCTCT 3060
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Qy 3121 CTCCTATCTTTGGGCTGATTAATCTCTCTCATTAATACATAAATTTCTGAAATTTTTC 3180
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Qy 3181 ACATAAACTACTAGAGCTACCTCACCATCTCTGTTTTTAAACGCGAGCAGTTTACTATATA 3240
Db 3181 ACATAAACTACTAGAGCTACCTCACCATCTCTGTTTTTAAACGCGAGCAGTTTACTATATA 3240
Qy 3241 ATTACTATTATAA 3253
Db 3241 ATTACTATTATAA 3253

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RESULT 3
US-09-016-000-8
; Sequence 8, Application US/09016000
; Patent No. 5962232
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Akerblom, Ingrid E.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; APPLICANT: Guesler, Karl G.
; TITLE OF INVENTION: PROTEIN KINASE MOLECULES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 1174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.000
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0465 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2791 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HEARNOT01
; CLONE: 307624
US-09-016-000-8

Query Match          79.8%; Score 2595.6; DB 2; Length 2791;
Best Local Similarity 97.0%; Pred. NO. 0;
Matches 2713; Conservative 0; Mismatches 14; Indels 69; Gaps 4

QY      15  GGAGGCTGCAGCCAGCTCGTCTCGGCGCCGCGCTGCGAGAGCCCGCCCGCG 74
DB      1  GGAGGCTGCAGCCAGCTCGTCTCGGCGCCGCGCTGCGAGAGCCCGCGCG 59
QY      75  CTTCCGCGCGCTCGGAATGAGCTCCCGAAAGTCTCGGCCATTACAGGCCGAAAGCGGAG 134
DB      60  CTTCCGCGCGCTCGGAATGAGCTCCCGAAAGTCTCGGCCATTACAGGCCGAAAGCGGAG 119
QY      135 GCCGAAAGAGAGAAAAACATCCGAAAAA-----GCCGGAGCCTCAACAGAAAGCTCTTTAG 190
DB      120 GCCGAAAGAGAGAAAAACATCCGAAAAAATCAACAGAGATTGAGCTGCTGATGTGAG 179
QY      162 -----GCCGGAGCCTCAACAGAAAGCTCTTTAG 190
DB      180 TTAAGCTCTGAGAAGTCGCTCTTTACAGAAAGCGCGAGCCTCAACAGAAAGCTCTTTAG 239

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1271 CCAATGGCCATATTGAGAAATGGCCCATCTTCTACCTGGAGCAGCAACTGAGCATGAAGATG 1330
1320 CCAATGGCCATATTGAGAAATGGCCCATCTTCTACCTGGAGCAGCAACTGAGCATGAAGATG 1379
1331 ATGATGAAGAAGACTGCGCCCAATCTGAGGAATATAATCTTGTAGTGAGCCAAATCGAGAAA 1390
1380 ATGATGAAGAAGACTGCGCCCAATCTGAGGAATATAATCTTGTAGTGAGCCAAATCGAGAAA 1439
1391 GTGATTAACATATAGCAGCTCTTANGAACTTCAATGGTGAATTTGCCAAATGGACGAC 1450
1440 GTGATTAACATATAGCAGCTCTTANGAACTTCAATGGTGAATTTGCCAAATGGACGAC 1499
1451 ATAAATTTCCCGAGTTCAGAGTTCCAGAGTTTCCAGCTCTGTTCTCTCTGATCTCTTAG 1510
1500 ATAAATTTCCCGAGTTCAGAGTTTCCAGAGTTTCCAGCTCTGTTCTCTCTGATCTCTTAG 1559
1511 AACCTGTGGCTCGCGCTCTGTGCTTCTGAGGGATCACCACTTCTAGCAAGAGGAGA 1570
1560 AACCTGTGGCTCGCGCTCTGTGCTTCTGAGGGATCACCACTTCTAGCAAGAGGAGA 1619
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1800 AAGACATCCAGCGGTGAGTACCGCTCCATAGAGTGTATATAGAGCGGGGTACAGCA 1859
1811 CCCCTCGGACATCTGGAGCAGCGGTGTATGGCATTGTGAGCTGGCAACGGGAGATTAT 1870
1860 CCCCTCGGACATCTGGAGCAGCGGTGTATGGCATTGTGAGCTGGCAACGGGAGATTAT 1919
1871 TGTGTAACACATCTTGGGGAAGACTATTCAGAGCAGAACACACATAGCCCAATCA 1930
1920 TGTGTAACACATCTTGGGGAAGACTATTCAGAGCAGAACACACATAGCCCAATCA 1979
1931 TAGAGCTGTAGGCAATTTCCAAAGCACTTTGCTCTATCTGGAATAATTTCTCGGAAT 1990
1980 TAGAGCTGTAGGCAATTTCCAAAGCACTTTGCTCTATCTGGAATAATTTCTCGGAAT 2039
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2111 TGATCCCGATTTAGAAATGGTTCCAGAAAAACGAGCCTCAGCTGGCGAATGCTTCGCG 2170
2160 TGATCCCGATTTAGAAATGGTTCCAGAAAAACGAGCCTCAGCTGGCGAATGCTTCGCG 2219
2171 ATCTTGGTTGAAATTTCTAGCAATTTCTACCAATATGCAATTTCTGAGCTAGCAAAATGTC 2230
2220 ATCTTGGTTGAAATTTCTAGCAATTTCTACCAATATGCAATTTCTGAGCTAGCAAAATGTC 2279
2231 CCAGTACATTTGGAACCTTAAACGGTGAATCTCAATTTCTTAAACAGGATTTACAGTGGC 2290
2280 CCAGTACATTTGGAACCTTAAACGGTGAATCTCAATTTCTTAAACAGGATTTACAGTGGC 2339
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2340 TTCACTCTCAGACCTTTATTTGCTTTGAGGTAATGTTGTTGCAATTTTCTTTTGTG 2399
2351 CACTGTGATCTGGGGAAGGGTAGTCTTTTGTCTTCTGAGCTAAGTAGTTTACTGACCAATTT 2410

2400 CACTGTGATCTCTGGGAAGGGTAGTCTTTTGTCTTCTCAGCTAAGTAGTTTACTGACCAATTT 2459
2411 TCTTCTGGAACAATAACATGCTCTTAAGCATTTTCTTGTGTTCTGTTGACATTTCAAAAT 2470
2460 TCTTCTGGAACAATAACATGCTCTTAAGCATTTTCTTGTGTTCTGTTGACATTTCAAAAT 2519
2471 GTCAATTTTTGAATGAAAAAATCTTTTCCCTTTTGTGTTTGGCAGGTTTGTAACTATT 2530
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2531 TATGAAGAAATATTTTAGCTGAGTACTATATAATTTTACAATCTTAAAGAAATTTCAAGTT 2590
2580 TATGAAGAAATATTTTAGCTGAGTACTATATAATTTTACAATCTTAAAGAAATTTCAAGTT 2639
2591 GGGACCAAGAAAAATAGCAAGGAAATGTACAAATTTTATCTTCTGGCAAGGGACATCAT 2650
2640 GGAACCAAGAAATA--GCAAGGAATGTACAAATTTTATCTTCTGGCAAGGGACATCAT 2696
2651 TCCTGTATTATAGTGTATGTAATGCAACCTGTAAATGTTTACTTTGGATTTAAATATGGGA 2710
2697 TCCTGTATTATAGTGTATGTAATGCAACCTGTAAATGTTTACTTTCCATTTAAATATGGGA 2756
2711 GGGGGGACTCAAAATTTTCAGAAAGCTTAAAAAATAA 2746
2757 -GGGGGACTCAAAATTTTCAGAAAGCTTAAAAAATAA 2791

RESULT 4
US-09-759-359A-3
; Sequence 3, Application US/09759359A
; Patent No. 6492153
; GENERAL INFORMATION:
; APPLICANT: ABU-THREIDBH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01043
; CURRENT APPLICATION NUMBER: US/09/759,359A
; CURRENT FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-09-759-359A-3

Query Match 20.5%; Score 666.2; DB 4; Length 90541;
Best Local Similarity 97.3%; Pred. No. 5.4e-155;
Matches 721; Conservative 0; Mismatches 13; Indels 7; Gaps 4;

QY 2004 AGGGAACCTGGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGGA 2063
DB 87810 AGGGAACCTGGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGGA 87869
QY 2064 AAGATATGCTGCGCCCATGAAGTGTGACAGTTTACAGATTTCTCGATCCCGATGTT 2123
DB 87870 AAGATATGCTGCGCCCATGAAGTGTGACAGTTTACAGATTTCTCGATCCCGATGTT 87929
QY 2124 AGAAATGTTCCAGAAAAACGAGCCTCAGCTGGCGAATGCTTGGCAATTCCTTGGTTGAA 2183
DB 87930 AGAAATGTTCCAGAAAAACGAGCCTCAGCTGGCGAATGCTTGGCAATTCCTTGGTTGAA 87989
QY 2184 TTCTTAGCAAAATTTACCAATTTTGCATTTCTGAGTAGCAAAATGTTCCAGTACATTTGGA 2243
DB 87990 TTCTTAGCAAAATTTACCAATTTTGCATTTCTGAGTAGCAAAATGTTCCAGTACATTTGGA 88049
QY 2244 CCTAAACGGTGAATCTCTATTTTAAACAGGATTTACAGTGGCTGGCTTCATCTCAGAC 2303
DB 88050 CCTAAACGGTGAATCTCTATTTTAAACAGGATTTACAGTGGCTGGCTTCATCTCAGAC 88109
QY 2304 CTTTATTTTGTCTTGGGTAAGTGTGTTGTTGACATTTTGTCTTTGTGCACTGTGATCTCTG 2363

Db 88110 CTTTATTTTGGCTTGGAGTACTGTTGTTTGACATTTTGGCTTTTGTGCACTGTGATCCTG 88169
QY 2364 GGGAGGGTGTGCTTTT--TGTCTTCTAGCTAAGTGTGTTTACTGACCAATTTTCTTT--CTGGAA 2420
Db 88170 GGGAGGGTGTGCTTTTGTGCTTCTAGCTAAGTGTGTTTACTGACCAATTTTCTTCTCTGGAA 88229
QY 2421 ACAATAACATGCTCTTAAGCATTTTCTTGTGTTGTGTTGACATTCAAATGTCAATTTT 2480
Db 88230 ACAATAACATGCTCTTAAGCATTTTCTTGTGTTGTGTTGACATTCAAATGTCAATTTT 88289
QY 2481 TGAATGAAAAATACATTTTCCCTTTTGTGTTTGGCAGGTTTGTAACTATTATTAAGAAA 2540
Db 88290 TGAATGAAAAATACATTTTCCCTTTTGTGTTTGGCAGGTTTGTAACTATTATTAAGAAA 88349
QY 2541 TATTTTAGCTGAGTACTATATAATTTTACAATCTTAAAGAAATTTATCAAGTTGGGAACCAAG 2600
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QY 2601 AAAATAGCAAGGAAATGACAAATTTTATCTTCTGCAAGGAGGACATCATCTCTGTATTA 2660
Db 88410 AATA---GCAAGAAATGACAAATTTTATCTTCTGCAAGGAGGACATCATCTCTGTATTA 88466
QY 2661 TAGTGTATGTAATGACCCCTGTAAATGTTTACTTTTGGATTAATAATGGAGGGGACTC 2720
Db 88467 TAGTGTATGTAATGACCCCTGTAAATGTTTACTTTCCATTAATAATGGAGGGGACTC 88525
QY 2721 AAATTTTCAGAAAAGCTAAAAA 2741
Db 88526 AAATTTTCAGAAAAGCTAACCA 88546

RESULT 5
US-10-207-973-3
; Sequence 3, Application US/10207973
; Patent No. 6753175
; GENERAL INFORMATION:
; APPLICANT: ASU-THREIDEH, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001043
; CURRENT APPLICATION NUMBER: US/10/207,973
; CURRENT FILING DATE: 2002-07-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 90541
; TYPE: DNA
; ORGANISM: Human
US-10-207-973-3

Query Match 20.5%; Score 666.2; DB 4; Length 90541;
Best Local Similarity 97.3%; Pred. No. 5.4e-155;
Matches 721; Conservative 0; Mismatches 13; Indels 7; Gaps 4;

QY 2004 AGGAGAACTGCGACACATCACCAGCTGAAGCCCTTGTGATGTACTTGTGTA 2063
Db 87810 AGGAGAACTGCGACACATCACCAGCTGAAGCCCTTGTGATGTACTTGTGTA 87869
QY 2064 AAGATATGCTGCCCCCATGAGATGCTGCACAGTTTACAGATTTTCCGATCCGATGTT 2123
Db 87870 AAGATATGCTGCCCCCATGAGATGCTGCACAGTTTACAGATTTTCCGATCCGATGTT 87929
QY 2124 AGAATATGTTTCCAGAAAAACGAGCCCTCAGCTGCGAATCCCTTGGCATCTTGGTTGAA 2183
Db 87930 AGAATATGTTTCCAGAAAAACGAGCCCTCAGCTGCGAATCCCTTGGCATCTTGGTTGAA 87989
QY 2184 TTCTTAGCAAAATTTTACCAATATTTGCAATCTGAGCTAGCAAAATGTTCCAGTACATTTGGA 2243
Db 87990 TTCTTAGCAAAATTTTACCAATATTTGCAATCTGAGCTAGCAAAATGTTCCAGTACATTTGGA 88049
QY 2244 CCTAAACGGTGAATCTCTCAATTTCTTTAAACAGGATTAACAGTGAGCTGGCTTCATCTCAGAC 2303

Db 88050 CTTAAACGGTGAATCTCTCAATTTTAAACAGGATTAACAGTGAGCTGGCTTCATCTCAGAC 88109
QY 2304 CTTTATTTTGTCTTGGAGTACTGTTGTTTGAATTTTGTCTTTTGTGCACTGTGATCCTG 2363
Db 88110 CTTTATTTTGTCTTGGAGTACTGTTGTTTGAATTTTGTCTTTTGTGCACTGTGATCCTG 88169
QY 2364 GGGAGGGTGTGCTTTT--TGTCTTCTAGCTAAGTGTGTTTACTGACCAATTTTCTTT--CTGGAA 2420
Db 88170 GGGAGGGTGTGCTTTTGTGCTTCTAGCTAAGTGTGTTTACTGACCAATTTTCTTCTCTGGAA 88229
QY 2421 ACAATAACATGCTCTTAAGCATTTTCTTGTGTTGTGTTGACATTCAAATGTCAATTTT 2480
Db 88230 ACAATAACATGCTCTTAAGCATTTTCTTGTGTTGTGTTGACATTCAAATGTCAATTTT 88289
QY 2481 TGAATGAAAAATACATTTTCCCTTTTGTGTTTGGCAGGTTTGTAACTATTATTAAGAAA 2540
Db 88290 TGAATGAAAAATACATTTTCCCTTTTGTGTTTGGCAGGTTTGTAACTATTATTAAGAAA 88349
QY 2541 TATTTTAGCTGAGTACTATATAATTTTACAATCTTAAAGAAATTTATCAAGTTGGGAACCAAG 2600
Db 88350 TATTTTAGCTGAGTACTATATAATTTTACAATCTTAAAGAAATTTATCAAGTTGGGAACCAAG 88409
QY 2601 AAAATAGCAAGGAAATGACAAATTTTATCTTCTGCAAGGAGGACATCATCTCTGTATTA 2660
Db 88410 AATA---GCAAGAAATGACAAATTTTATCTTCTGCAAGGAGGACATCATCTCTGTATTA 88466
QY 2661 TAGTGTATGTAATGACCCCTGTAAATGTTTACTTTTGGATTAATAATGGAGGGGACTC 2720
Db 88467 TAGTGTATGTAATGACCCCTGTAAATGTTTACTTTCCATTAATAATGGAGGGGACTC 88525
QY 2721 AAATTTTCAGAAAAGCTAAAAA 2741
Db 88526 AAATTTTCAGAAAAGCTAACCA 88546

RESULT 6
US-08-264-002-1
; Sequence 1, Application US/08264002
; Patent No. 5859019
; GENERAL INFORMATION:
; APPLICANT: GUI, JIAN-PANG
; APPLICANT: FU, XIANG-DONG
; TITLE OF INVENTION: NOVEL PROTEIN SERINE KINASE, SRPK1
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
; STREET: 1880 Century Park East, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,002
; FILING DATE: 22-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: TUMARKIN PH.D., LISA A.
; REGISTRATION NUMBER: P-38,347
; REFERENCE/DOCKET NUMBER: PD3590
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/455-5100
; TELEFAX: 619/455-5110
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

RESULT 7

US-09-016-434-703
; Sequence 703, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 703:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 923 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HEARNOT01
; CLONE: 307624
US-09-016-434-703

Query Match 19.3%; Score 629.4; DB 4; Length 923;
Best Local Similarity 88.3%; Pred. No. 5.7e-147;
Matches 700; Conservative 0; Mismatches 89; Indels 4; Gaps 3;
QY 157 AAAAAAGCGGAGCCTCAACAGAAAGCTCTTTAGTTCTCTCTCCACCGGCACACCA 216
DB 43 AAAAAAGCGGCGCCCTGGCCAAAGCTCANTTTTCTCTCTCCACCGGCACACCA 102
QY 217 CCACACCGCCACCTTTTCCAGACCCACACCCCGGAGCCAGAGAGAGATCTCGGA 276
DB 103 CCACACCGCCNCTTTTCGCGACCCACACCCCGGAGCCAGAGAGAGATCTCGGA 162
QY 277 TCAGATGATGAGGAGCAGAGACCTCTCGGACTACTCAAGAGTGGATATCATCATG 336
DB 163 TCAGATGATGAGGAGCAGAGACCTCTCGGACTACTCNCANTGTGGATATCATCATG 222
QY 337 AAAAAAGGAGACCTTCAATGCGCGGTATCATGTTATTAGAAAGCTTGGATGGGGCAC 396
DB 223 AAAAAAGGAGACCTTCAATGCGCGGTATCATGTTATTAGAAAGCTTGGATGGGGCAC 282
QY 397 TTCTCTACTGTGCTGTGCTGGATATGCGGGGAAAGATTGTTGCAATGAAGTT 456
DB 283 TTCTCTACTGTGCTGTGCTGGATATGCGGGGAAAGATTGTTGCAATGAAGTT 342
QY 457 GTAAAAAGTGGCCAGCATTTATACGGAGACAGCCCTTGGATGAAATTAATTTGCTCAATGT 516

DB 343 GTAAAAAGTGGCCAGCCTTTTNTGATACAGCCTTGGATGAAATTAATTTGCTCAATGT 402
QY 517 GTTCGAGAAAGTGATCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATTTGACGAC 576
DB 403 GTTCGAGAAAGTGATCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATTTGACGAC 462
QY 577 TTCAAGATTTTCAGGCATGAATGGGATACATGCTGTCATGGTCTTGAAGTACTTTGGCCAC 536
DB 463 TTTAAGATTTTCAGGCATGAATGGGATACATGCTGTCATGGTCTTGAAGTACTTTGGCCAC 522
QY 637 CATCTCCTCAAGTGATCATCAATCCAACTATCAAGGCTCCCAAGTACTTTGTTGAAG 696
DB 523 CATCTCCTCAAGTGATCATCAATCCAACTATCAAGGCTCCCAAGTACTTTGTTGAAG 582
QY 697 AGTATCATTCGACAGGCTCTTCAAGGTTAGATTACTTACACAGTAAG-TGCAAGATCAT 755
DB 583 AGTATCATTCGACAGGCTCTTCAAGGTTAGATTACTTACACAGTAAGTTGCAAGATCAT 642
QY 756 TCATCTGACATAAAGCCGGAATAATCTTGTGATGTTGTGGATGATGATGATGAGAG 815
DB 643 ACNTACTGACATAAAGCCGGAATAATCTTGTGATGTTGTGNGAAGANGCATATTTAANAAG 702
QY 816 AATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTCTCTCTCTTTCAGGGTCTGC 875
DB 703 AATGGCAGCTGANG--CCCTGATTGCAANAAGCAGGTGCTCC-NCTCCCTCAGGGTCTGC 759
QY 876 AGTGAGTACGGCTCCACAGCAGAAACCTATAGGAAAAATATCTAAAAACAAAAAGAAAA 935
DB 760 ANTGAATTACGGTCCCGCNGCAAACTTNGGAAAAATTTCTAAACCCNNNGAAAAACTGA 819
QY 936 ACTGAAAAAGAAA 948
DB 820 AANAACCCNAAAA 832

RESULT 8

US-09-173-581-10
; Sequence 10, Application US/09173581A
; Patent No. 6013455
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Yalda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PF-0614 US
; CURRENT APPLICATION NUMBER: US/09/173,581A
; CURRENT FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 119819
US-09-173-581-10

Query Match 9.0%; Score 293.4; DB 3; Length 1427;
Best Local Similarity 69.8%; Pred. No. 4.3e-63;
Matches 396; Conservative 0; Mismatches 171; Indels 0; Gaps 0;
QY 1624 TTGCCAAAGCAAAAACCCGGGACGTGACTTGTGTTGGTGAATCCCTCGGATCCGCGAAT 1683
DB 800 TCGCCTAGCACACCATTCGGTGGCTCGAACCTCTCTGGTGAACCCCTCGAGCCCCCAAT 859
QY 1684 GCAGATAAATTAGAGTAAAAATTCCTGACCTGGGAAATGCTTGTGGGTGCATTAACAC 1743

Db 860 GCAGATAAGATCAAGATCGAGACCTGGGCAACGCTCTGGTGCGCAAGCAC 919
Qy 1744 TTCACGGAAGACATCCAGACCGCTCAGTACCGCTCCATAGAGTTTAAATAGGAGCGGG 1803
Db 920 TTCACGGAAGACATCCAGACCTGGGCAACGCTCTGGTGCGCAAGCAC 979
Qy 1804 TACAGCACCTCGGAGACATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1863
Db 980 TACGGCCCCCGGAGACATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1039
Qy 1864 GATTATTTGTTGAACCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1923
Db 1040 GACTACCTGTTGAGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1099
Qy 1924 CACATATAGAGCTGTAGGAGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1983
Db 1100 CACTAGTGGAGCTTCTGGGAGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1159
Qy 1984 CGGGAATTTCTCAATCGCAGAGGAGAACTGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 2043
Db 1160 CGGGAATTTCTCAATCGCAGAGGAGAACTGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1219
Qy 2044 CTCTTTGATGTTCTCAATCGCAGAGGAGAACTGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 2103
Db 1220 CTGTACGAGTACTCATGGAAGAGTACGAGTGGGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1279
Qy 2104 GATTTCCTGATCCGAGTGTGAATGTTCCAGAAAAACGAGCTTACGCTGGCGAATGC 2163
Db 1280 GCCTTTCTGCTGCCATGAATGATGATACATCCCGGAAAGCGGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1339
Qy 2164 CTTCGGCATCCTGTTGATTTCTTAG 2190
Db 1340 CTCAGCACCCCTGGCTCCAAACCTAG 1366

RESULT 9

US-09-420-915-10
; Sequence 10, Application US/09420915
; Patent No. 6264947
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; APPLICANT: Guebler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gorgone, Gina
; APPLICANT: Azimzai, Valda
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: Protein Kinase Homologs
; FILE REFERENCE: PR-0614 US
; CURRENT APPLICATION NUMBER: US/09/420,915
; CURRENT FILING DATE: 1999-10-20
; EARLIER FILING DATE: 1998-10-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 1427
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 119819
US-09-420-915-10

Query Match 9.0%; Score 293.4; DB 3; Length 1427;
Best Local Similarity 69.8%; Pred. No. 4.3e-63;
Matches 396; Conservative 0; Mismatches 171; Indels 0; Gaps 0;
Qy 1624 TTGCCAAAGCAAAACCCGGGAGCTGACATGTTGGTGAATCCCTGGATCCCGGAAT 1683
Db 800 TCGCCTAGCACACCATTCGGTCCGCTCGAACCTCTCGTGTGAACCCCTGGAGCCCAAAAT 859

Qy 1684 GCAGATAAATTTAGATTAATAATTTGCTGACTGGAAATGCTTGTGGTGCATTAACAC 1743
Db 860 GCAGATAAGATCAAGATCAAGATCGAGACCTGGGCAACGCTCTGGTGCGCAAGCAC 919
Qy 1744 TTCACGGAAGACATCCAGACCGCTCAGTACCGCTCCATAGAGTTTAAATAGGAGCGGG 1803
Db 920 TTCACGGAAGACATCCAGACCTGGGCAACGCTCTGGTGCGCAAGCAC 979
Qy 1804 TACAGCACCTCGGAGACATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1863
Db 980 TACGGCCCCCGGAGACATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1039
Qy 1864 GATTATTTGTTGAACCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1923
Db 1040 GACTACCTGTTGAGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1099
Qy 1924 CACATATAGAGCTGTAGGAGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1983
Db 1100 CACTAGTGGAGCTTCTGGGAGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1159
Qy 1984 CGGGAATTTCTCAATCGCAGAGGAGAACTGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 2043
Db 1160 CGGGAATTTCTCAATCGCAGAGGAGAACTGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1219
Qy 2044 CTCTTTGATGTTCTCAATCGCAGAGGAGAACTGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 2103
Db 1220 CTGTACGAGTACTCATGGAAGAGTACGAGTGGGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1279
Qy 2104 GATTTCCTGATCCGAGTGTGAATGTTCCAGAAAAACGAGCTTACGCTGGCGAATGC 2163
Db 1280 GCCTTTCTGCTGCCATGAATGATGATACATCCCGGAAAGCGGCGGCAATTCGAGACCGGCTGTATGGCAATTTGAGCTGGCAACGGGA 1339
Qy 2164 CTTCGGCATCCTGTTGATTTCTTAG 2190
Db 1340 CTCAGCACCCCTGGCTCCAAACCTAG 1366

RESULT 10

US-09-016-434-79
; Sequence 79, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:

```

; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 793 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: MUSCNOT01
; CLONE: 119819
US-09-016-434-79

Query Match 7.8%; Score 254; DB 4; Length 793;
Best Local Similarity 67.4%; Pred. No. 2e-53; Indels 2; Gaps 2;
Matches 360; Conservative 0; Mismatches 172;

QY 269 TCCTGGGATCAGATGATGAGGAGGAGGACCTCGGACTACTGCAAGAGGTGGATATC 328
DB 156 TTCTGGGCTCCGACGAGGAGAACAGGAGACCCCAAGACTACTGCAAGGCGGCTACC 215
QY 329 ATCCAGTGAATTTGAGACCTCTTCAATGGCGGTATCATGTTATTAGAAAGCTTGGAT 388
DB 216 ACCCTGTGAAGATCGCGGACGTGTTCAATGGCGGTACCACGTGTGCNCCNCCNGCT 275
QY 389 GGGGCGACTCTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 448
DB 276 GGGGCGACTCTCTCCACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 335
QY 449 TGAAAGTTGTAAAGAGTCCGACGACTTATAC -GGAGACAGCCTTGGATGAATAAAATTG 507
DB 336 TCAAGTGTGAAGTGGCGGCACTTACACGGGAGACAGCTGTGGATGAATCAANTC 395
QY 508 CT -CAAAATGTTTCGAGAAAGTGATCCAGTACCCCAACCAAGACATGTTGGTCCAGT 566
DB 396 CTGAAATGTTGTCGGGACAGGACCCAGTACCCCAAGAAAGAACCATTTGTCANCT 455
QY 567 CATTGACGACTTCAAGATTTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 626
DB 456 CATTGATGACTTCAGATCTCANGAGTCAATGANTCCATGTTGTCATGTTGCTGGANGT 515
QY 627 ACTTGGCCACCATCTCTCAAGTGGATCATCAAACTCAACTATCAAGGCTCCCAAGTAGG 686
DB 516 GCTGGGCCACCACTCTCTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 575
QY 687 TTGTGTGAAGATGATCATTCGACAGTCTCTCAAGGGTTAGATTACTTACACAGTAAGTG 746
DB 576 CTGCCTTNAANAACATCTNANGANGTGTCTGCACNGCTGNANTACCCACACCONANTTG 635
QY 747 CAAGATCATCTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 800
DB 636 CAANATCTNCCACNCGGAATCAANCCCCCAAAACATCTTTGCTGTGTGTGGGGGA 689
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RESULT 11
US-09-016-434-808
; Sequence 808, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 808:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 249 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAINOT03
; CLONE: 529450
US-09-016-434-808

Query Match 7.6%; Score 248; DB 4; Length 249;
Best Local Similarity 99.6%; Pred. No. 3.3e-52;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1601 TTTGAGCCTCCAGTACTCGGGATTTGCCAAAGCAAAACCCGGGCGAGCTGACTTTGG 1660
DB 1 TTTGAGCCTCCAGTACTCGGGATTTGCCAAAGCAAAACCCGGGCGAGCTGACTTTGG 60
QY 1661 TGAATCCCTCGATCCGCGGAATGCAGATAAAATTAGAGTAAAAATTGCTGACCTGGGA 1720
DB 61 TGAATCCCTCGATCCGCGGAATGCAGATAAAATTAGAGTAAAAATTGCTGACCTGGGA 120
QY 1721 ATGCTTTGTTGGTGCATAAAACACTTCACGGAAGACATCCAGACGGTCACTGACCTCCA 1780
DB 121 ATGCTTTGTTGGTGCATAAAACACTTCACGGAAGACATCCAGACGGTCACTGACCTCCA 180
QY 1781 TAGAGTTTTTAATAGGAGCGGGGTACAGCACCCCTCGGACATCTGGAGCACGGGTGTA 1840
DB 181 TAGAGTTTTTAATAGGAGCGGGGTACAGCACCCCTCGGACATCTGGAGCACGGGTGTA 240
QY 1841 TGGCATTTG 1849
DB 241 TGGCATTTG 249
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RESULT 12
US-09-385-982-396
; Sequence 396, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: II
; FILE REFERENCE: CCNDA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
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; SEQ ID NO 6406
; LENGTH: 1731
; TYPE: DNA
; ORGANISM: Ca
US-09-248-796A-6

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Query Match 4.9%; Score 159.2; DB 4; Length 1731;
Best Local Similarity 55.7%; Pred. No. 1.4e-29;
Matches 305; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

RESULT 15

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RESULT 15
US-09-270-767-1008
; Sequence 1008, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1008
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1008

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Query Match 3.6%; Score 117; DB 4; Length 569;
Best Local Similarity 67.3%; Pred. No. 2.4e-19;
Matches 165; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Search completed: January 23, 2005, 11:11:32
Job time : 258.768 secs

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OM nucleic - nucleic search, using sw model

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1: January 23, 2005, 03:34:58 ; Search time 1468.41 Seconds
    (without alignments)
    11629.152 Million cell updates/sec

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Title: US-10-799-676-1
Perfect score: 3253
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

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Minimum DB seq length: 0
Maximum DB seq length: 20
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
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6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*
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SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	3253	100.0	3253	10	ADJ37688	Adj37688 Human kin
2	3249.8	99.9	3253	6	ABS52846	ABS52846 cDNA enco
3	2595.6	79.8	2791	2	AX89851	AX89851 Human pro
4	2333.8	77.9	3702	8	ALU54214	ALU54214 SR protei
5	2533.8	77.9	3715	12	ADJ96579	AdJ96579 Human SRP
6	2497	76.8	3745	6	ABK51173	ABK51173 cDNA enco
7	2497	76.8	3745	8	ADK53129	ADK53129 Human DNA
8	2497	76.8	3745	8	ALU54215	ALU54215 SR protei
9	2497	76.8	3745	12	ADO19346	ADO19346 Human PRO
10	2039.6	62.7	2094	8	ALU54217	ALU54217 SR protei
11	1753.6	53.9	1956	8	ALU54216	ALU54216 SR protei
12	1237	38.0	3213	5	AS566342	AS566342 DNA enco
13	712.8	21.9	1005	12	ADN98453	ADN98453 Novel hum
14	712.8	21.9	1005	12	ADO00022	ADO00022 Novel hum
15	709.6	21.2	1017	8	ALU54219	ALU54219 SR protei
16	689.2	21.2	113033	8	ALU54213	ALU54213 SR protei
17	666.2	20.5	90541	10	ADJ37690	AdJ37690 Human kin
18	664.6	20.4	90541	6	ABS52847	ABS52847 Human SR
19	636.4	19.6	4392	5	AS578896	AS578896 DNA enco
20	632.8	19.5	4326	6	ABK84213	ABK84213 Human cDN
21	632.8	19.5	4326	6	ABN96797	ABN96797 Gene #329

ALIGNMENTS

RESULT 1

ADJ37688
ID ADJ37688 standard; cDNA; 3253 BP.

AC ADJ37688;

DT 06-MAY-2004 (first entry)

Human kinase cDNA.

KW Kinase protein; drug screening assay; gene therapy;

pharmacogenomic analysis; testis; nervous tissue; fetal; lung; kidney protein; drug screening assay; gene therapy

brain anaplastic oligodendroglioma; lung carcinoid tissue; KW

KW soft tissue leiomyosarcoma; ovary tumour tissue; germ cell tumour tissue;

KW transgenic animal; human; gene; ss.

OS Homo sapiens.

	Key	Location/Qualifiers
FH		

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FT /*tag= a

FT	CDS	91.2190
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FT /*tag= b

$$\text{FT} \quad \text{product} =$$

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16-JAN-2001; 200103-0

PA (APPL-) APPLERA CORP.
XX

FI
yy
Abu-Threiden J, Gon

XX
DP WPT: 2003-899544/82

DR p-PSDB; ADJ37689.
yy

XX DE New: some ideas would be added to a higher level of a system of a family, useful for a variety of

PT	testis, nervous tissue, fetal, lung, ovary tumor tissue.	
XX	Claim 4; SEQ ID NO 1; 102pb; English.	
PS	The present invention relates to kinase protein and nucleotides encoding	
XX	them. The invention is useful in drug screening assays, tissue typing,	
CC	gene therapy and pharmacogenomic analysis. They are also useful in	
CC	treating disorders associated with the absence of, inappropriate, or	
CC	unwanted expression of kinase protein in testis, nervous tissue, fetal,	
CC	lung, brain anaplastic oligodendrogloma, lung carcinoma tissue, soft	
CC	tissue leiomyosarcoma, ovary tumour tissue, or germ cell tumour tissue.	
CC	The invention are useful as models for the development of human	
CC	therapeutic targets, aid in the identification of therapeutic proteins	
CC	and serve as targets for the development of human therapeutic agents that	
CC	modulate protease activity in cells and tissues that express the kinase	
CC	peptide. The invention is also useful in producing a kinase protein or	
CC	peptide, and non-human transgenic animals. The present sequence is human	
XX	kinase cDNA.	
XX	Sequence 3253 BP; 991 A; 693 C; 723 G; 846 T; 0 U; 0 Other;	
SQ	Query Match 100.0%; Score 3253; DB 10; Length 3253;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 3253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TCGCGGAGCGAGTGGAGCTGCAGCCAGCTCGTCTGGCGCCGCGTGCCTCGCGA 60	721 GGGTTAGATTACTTACACAGTAAGTCAAGATCATTTATACATACATATAAGCCGGAAT 780
DB	1 TCGCGGAGCGAGTGGAGCTGCAGCCAGCTCGTCTGGCGCCGCGTGCCTCGCGA 60	721 GGGTTAGATTACTTACACAGTAAGTCAAGATCATTTATACATACATATAAGCCGGAAT 780
QY	61 AGCCCCCGCCCGCTTCGCGCGCGTCCGGAATGAGCTCCCGGAAAGTGTGSCCAATCAG 120	781 ATCTTGATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
DB	61 AGCCCCCGCCCGCTTCGCGCGCGTCCGGAATGAGCTCCCGGAAAGTGTGSCCAATCAG 120	781 ATCTTGATGTGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY	121 GCCCGAAGCGGAGCGCGAAGAGAGAAACATCCGAAAGCCGAGGCTCAACAGAA 180	841 CAGAAAGCAGGTCT 900
DB	121 GCCCGAAGCGGAGCGCGAAGAGAGAAACATCCGAAAGCCGAGGCTCAACAGAA 180	841 CAGAAAGCAGGTCT 900
QY	181 GCTCCCTTAGTCTCTCTCTCCAGCCGACACACACACACACACACACACACACAC 240	901 CCTATAGGAAAAATATCTAAAAACAAAAAATACTGAAAGAAAAACAGAGAGCGAG 960
DB	181 GCTCCCTTAGTCTCTCTCTCCAGCCGACACACACACACACACACACACACACAC 240	901 CCTATAGGAAAAATATCTAAAAACAAAAAATACTGAAAGAAAAACAGAGAGCGAG 960
QY	241 CCCACACCCCGGAGCCAGAGGAGATCTGGGATCAGATGATGAGGAGCAAGAGGAC 300	961 GCTGAGTTATTGGAGAGCGCTGCGAGGAGATGAGAAATTGGAGCGAGAGCTGAAGG 1020
DB	241 CCCACACCCCGGAGCCAGAGGAGATCTGGGATCAGATGATGAGGAGCAAGAGGAC 300	961 GCTGAGTTATTGGAGAGCGCTGCGAGGAGATGAGAAATTGGAGCGAGAGCTGAAGG 1020
QY	301 CTTGGGACTCTGCAAGGTGATATCATCCAGTGAATAATGGAGACCTCTTCAATGCG 360	1021 AATAATAGAGAAAAATCATCCTCAGCTGCACCTTCCCAATCACAGGATGCGAATAC 1080
DB	301 CTTGGGACTCTGCAAGGTGATATCATCCAGTGAATAATGGAGACCTCTTCAATGCG 360	1021 AATAATAGAGAAAAATCATCCTCAGCTGCACCTTCCCAATCACAGGATGCGAATAC 1080
QY	361 CGGTATCATGTTATTAGAAAGCTTGGATGGGGGACCTTCTACTGTCTGGCTGTCTGG 420	1081 TGCCAGAGGTGAAACTTAAAAACAAACAGGATTAGAGAGCGCTGAGGAGAGACTGCA 1140
DB	361 CGGTATCATGTTATTAGAAAGCTTGGATGGGGGACCTTCTACTGTCTGGCTGTCTGG 420	1081 TGCCAGAGGTGAAACTTAAAAACAAACAGGATTAGAGAGCGCTGAGGAGAGACTGCA 1140
QY	421 GATATGAGGGGAAAGATTGTTGCAATGAAGTTGTAAAGTCCAGCAGCATTTATAG 480	1141 AAGGACAACTGTTGAAGCTGAGGAGCCAGGAGAGAAAGAAAGTGTGAGAAAGAAACATT 1200
DB	421 GATATGAGGGGAAAGATTGTTGCAATGAAGTTGTAAAGTCCAGCAGCATTTATAG 480	1141 AAGGACAACTGTTGAAGCTGAGGAGCCAGGAGAGAAAGAAAGTGTGAGAAAGAAACATT 1200
QY	481 GAGACAGCTTGGATGAATAAATTCCTCAATGTTGTCGAGAAAGTGCATCCAGTGAC 540	1201 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
DB	481 GAGACAGCTTGGATGAATAAATTCCTCAATGTTGTCGAGAAAGTGCATCCAGTGAC 540	1201 GAAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1260
QY	541 CCAACCAAGAGCATGGTGGTCCAGCTCATTTGACGACTTCAAGATTTTCAGGCAATGGG 600	1261 TCACCTAAACCAATGCGCATTTGAGAAATGGCCATTTCTCAGTGGAGAGCAACTGGAC 1320
DB	541 CCAACCAAGAGCATGGTGGTCCAGCTCATTTGACGACTTCAAGATTTTCAGGCAATGGG 600	1261 TCACCTAAACCAATGCGCATTTGAGAAATGGCCATTTCTCAGTGGAGAGCAACTGGAC 1320
QY	601 ATACATGTCTGATGCTTTCGAGTACTTGGCCACCATCTCTCAAGTGCATCAAA 660	1321 GATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
DB	601 ATACATGTCTGATGCTTTCGAGTACTTGGCCACCATCTCTCAAGTGCATCAAA 660	1321 GATGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380
QY	661 TCCAACTATCAAGGCTCCCAAGTACGTTGTGGAAGAGATATCATTCGACAGGCTCTTCAA 720	1381 AATGAGAAAGTGAATTACACATATAGCAGCTCTTGAACAAATTCATGTTGAATTGCGCA 1440
DB	661 TCCAACTATCAAGGCTCCCAAGTACGTTGTGGAAGAGATATCATTCGACAGGCTCTTCAA 720	1381 AATGAGAAAGTGAATTACACATATAGCAGCTCTTGAACAAATTCATGTTGAATTGCGCA 1440

1801 GGGTACAGACCCCTCGGACATCTGGAGCAGCGGTGTATGGCATTTGAGCTGGCAAG 1860
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1921 GCCCAGATCATAGAGCTGTAGGAGTATTTCCAGGCACTTTGCTCTATCTGGAAATAT 1980
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1981 TCTCGGGAATTTCTTCAATCGCAGAGAGAACTGCGACACATCACCAAGCTGAAGCCCTGG 2040
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2101 ACAGATTTCTGATCCCGATGTTAGAAATGTTTCCAGAAACAGAGCCTCAGTGGCGAA 2160
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2281 GTGAGTGGCTTCATCTCAGACCTTATTTGCTTTGAGGTACTGTGTTTGACATTTT 2340
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2401 CTGACCATTTCTTCTGGAACCAATAACATGCTCTTAAGCAATGTTTCTTGTGTTGTG 2460
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3181 ACATAAACTACTAGAGTACCTCACCATCTCTGTTTTTAAACGCGAGCAGTTACTATATA 3240
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3241 ATTACTATTATAA 3253
3241 ATTACTATTATAA 3253
RESULT 2
ABS52846
ID ABS52846 standard; cDNA; 3253 BP.
XX
AC ABS52846;
XX
DT 20-NOV-2002 (first entry)
XX
DE cDNA encoding human SR protein-specific kinase 2, SRPK2.
XX
KW Human; kinase; SRPK2; SR protein-specific kinase 2; gene; ss.
XX
OS Homo sapiens.
XX
EH Key Location/Qualifiers
FT 5'UTR 1..90
FT CDS /*tag= a
FT 91..2190
FT /*tag= b
FT /*product= "SR protein-specific kinase 2 (SRPK2) kinase"
FT 3'UTR 2190..3253
FT /*tag= c
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PN US2002094560-A1.
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PD 18-JUL-2002.
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PF 16-JAN-2001; 2001US-00759359.
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XX 16-JAN-2001; 2001US-00759359.
XX
XX (ABUT/) ABU-THREIDEH J.
XX (GONG/) GONG F.
XX (KETCHUM K A.) KETCHUM K A.
XX (DI FRANCESCO V.) DI FRANCESCO V.
XX (BEASLEY E M.) BEASLEY E M.
XX
XX Abu-Threideh J, Gong F, Ketchum KA, Di Francesco V, Beasley EM;
XX WPI; 2002-681805/73.
XX P-PSDB; ABG32447.
XX
XX New SR protein-specific kinase 2 peptides and nucleic acid sequences,
XX useful as models for developing human therapeutic targets, in identifying
XX therapeutic proteins, and in identifying agents that modulate kinase
XX activity.


```
QY 1741 CACTTCAGCGAAGACATCCAGACGCGTCAGTACCGCTCCATAGAGGCTTTTAATAGGAGCG 1800
Db 1741 CACTTCAGCGAAGACATCCAGACGCGTCAGTACCGCTCCATAGAGGCTTTTAATAGGAGCG 1800
QY 1801 GGGTACAGCACCCCTCGGACATCTGGAGCACGCGCTGTATGGCAATTTGAGCTGGCAACG 1860
Db 1801 GGGTACAGCACCCCTCGGACATCTGGAGCACGCGCTGTATGGCAATTTGAGCTGGCAACG 1860
QY 1861 GGGATATTTGTTGAAACACATCTGGGGAAGACTATTCGAGACGAGAACACACATA 1920
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QY 1921 GCCCAGCATATGAGCTGTAGGAGTATTTCCAAAGGCACTTTGCTCTATCTGGAATAT 1980
Db 1921 GCCCAGCATATGAGCTGTAGGAGTATTTCCAAAGGCACTTTGCTCTATCTGGAATAT 1980
QY 1981 TCTCGGGAATTTCTCAATCGCAGAGGAGAACTCGGACACATCAACCAAGCTGAAGCCCTGG 2040
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Db 2101 ACAGATTTCTGATCCGATGTTAGAAATGTTTCCAGAAACGAGCCCTCAGCTGCGGAA 2160
QY 2161 TGCCTTCGGCATCTTGGTGGTGAATTTCTAGCAAAATCTACCAATATTTGCATTTCTGAGCTA 2220
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QY 2401 CTGACCATTTTCTTCTGGAAACAAATTAACATGCTCTAAGCATGTTTCTGTGTTGTGG 2460
Db 2401 CTGACCATTTTCTTCTGGAAACAAATTAACATGCTCTAAGCATGTTTCTGTGTTGTGG 2460
QY 2461 ACATTCBAATGTGATTTTGTGAATGAAATACTTTCCCTTTGTTGTTTGGCAGGTTT 2520
Db 2461 ACATTCBAATGTGATTTTGTGAATGAAATACTTTCCCTTTGTTGTTTGGCAGGTTT 2520
QY 2521 TGTAACTATTTATGAAGAAATATTTTAGCTGAGTACTATATATTTTACAATCTTAAGAAA 2580
Db 2521 TGTAACTATTTATGAAGAAATATTTTAGCTGAGTACTATATATTTTACAATCTTAAGAAA 2580
QY 2581 TTATCAAGTTGGGAACCAAGAAATAGCAGGGAATGTACAATTTTATCTTCTGSCAAA 2640
Db 2581 TTATCAAGTTGGGAACCAAGAAATAGCAGGGAATGTACAATTTTATCTTCTGSCAAA 2640
QY 2641 GGGACATCATCTCTGATTTATAGTGTATGTAATGACCCCTGTAAATGTTTGGATT 2700
Db 2641 GGGACATCATCTCTGATTTATAGTGTATGTAATGACCCCTGTAAATGTTTGGATT 2700
QY 2701 AAATATGGAGGGGGGACTCAAAATTTAGAAAGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGG 2760
Db 2701 AAATATGGAGGGGGGACTCAAAATTTAGAAAGCTTAAAGGCTTAAAGGCTTAAAGGCTTAAAGG 2760
QY 2761 AAAAATFACTTTATATTAATAACCTTTCTTTGTTTTTTGTTTTTCTTATTTTCAATTT 2820
Db 2761 AAAAATFACTTTATATTAATAACCTTTCTTTGTTTTTTGTTTTTCTTATTTTCAATTT 2820
QY 2821 ATTAAATACACTTAACGTTGCGAAGCACTATGAAAAAATTAATACCATGAAAGGATCA 2880
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Db 2821 ATTAAATACACTTAACGTTGCGAAGCACTATGAAAAAATTAATACCATGAAAGGATCA 2880
QY 2881 AAAATCATAAATCAAAACCCCACTATAGTCCAACGACAAATTCATTCTCGGCGGTCAACTT 2940
Db 2881 AAAATCATAAATCAAAACCCCACTATAGTCCAACGACAAATTCATTCTCGGCGGTCAACTT 2940
QY 2941 TTTAAACATCTTATATAGTACCTGAGACTCTGGTCTCAATATTAATATCTAAATCTAC 3000
Db 2941 TTTAAACATCTTATATAGTACCTGAGACTCTGGTCTCAATATTAATATCTAAATCTAC 3000
QY 3001 CACCAAGTTAGGCCGCTAATGCTCTCTCGTGAATCTGTCATACAAATACATTTTCT 3060
Db 3001 CACCAAGTTAGGCCGCTAATGCTCTCTCGTGAATCTGTCATACAAATACATTTTCT 3060
QY 3061 ATTTATTTAGTGGTCTCGTTTATCTTTTCCGCCACATCTTTGTTCACTATTTTCTAGTTA 3120
Db 3061 ATTTATTTAGTGGTCTCGTTTATCTTTTCCGCCACATCTTTGTTCACTATTTTCTAGTTA 3120
QY 3121 CTCTTATCTTTGGCTGATTAAATCCTTCTCATATATCTCATATAAACTTCTGAAATTTTC 3180
Db 3121 CTCTTATCTTTGGCTGATTAAATCCTTCTCATATATCTCATATAAACTTCTGAAATTTTC 3180
QY 3181 ACATAAACTACTAGAGTACCTCACCATCTCTGTTTTTAAACGCGAGCAGTTACTATATA 3240
Db 3181 ACATAAACTACTAGAGTACCTCACCATCTCTGTTTTTAAACGCGAGCAGTTACTATATA 3240
QY 3241 ATTACTATTTAAA 3253
Db 3241 ATTACTATTTAAA 3253

RESULT 3
AAx89851
ID: AAX89851 standard; cDNA; 2791 bp.
XX
AC AAX89851;
XX
DT 08-OCT-1999 (first entry)
XX
DE Human protein kinase (HPKM)-2 encoding nucleotide (clone ID 307624).
XX
KW Human protein kinase molecule; HPKM; human; protein kinase;
KW phosphate group; cancer; immune disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 173..2239
FT /tag= a
FT /product= "HPKM-2"
XX
PN WO9338981-A2.
XX
PD 05-AUG-1999.
XX
PF 12-JAN-1999; 99WO-US0000661.
XX
PR 30-JAN-1998; 98US-00016000.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Hillman JL, Lal P, Akerblom IE, Shah P, Corley NC;
PI Guegler KJ;
XX
PI WPI: 1999-479190/40.
DR P-PSDB; AAY27053.
XX
PT New human protein kinase molecules useful for treating or preventing
PT cancer or an immune disorder.
XX
PS Claim 8; Page 73-74; 77pp; English.
XX
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QY 1931 TAGAGCTGTAGGACGATTTTCAAGGCACCTTTGCTCTATCTGGAATAATTTCTCGGAAT 1990
 DB 1980 TAGAGCTGTAGGACGATTTTCAAGGCACCTTTGCTCTATCTGGAATAATTTCTCGGAAT 2039
 QY 1991 TCTTCAATCCGAGAGAGAACTGCGACACATCAACCAAGCTGAGCCCTCGAGCCTCTTTG 2050
 DB 2040 TCTTCAATCCGAGAGAGAACTGCGACACATCAACCAAGCTGAGCCCTCGAGCCTCTTTG 2099
 QY 2051 ATGTACTTGTGGAAGATGCTGCGCCCATGAGATGCTGACAGATTTTACAGATTTC 2110
 DB 2100 ATGTACTTGTGGAAGATGCTGCGCCCATGAGATGCTGACAGATTTTACAGATTTC 2159
 QY 2111 TGATCCCGATGTTAGAAATGTTTCCAGAAAAACGAGCCTCAGCTGGCGAATGCTTCGCG 2170
 DB 2160 TGATCCCGATGTTAGAAATGTTTCCAGAAAAACGAGCCTCAGCTGGCGAATGCTTCGCG 2219
 QY 2171 ATCTTTGGTGAATCTTAGCAAAATTTCAACAAATTTGCAATTTGAGCTAGCAAAATGTT 2230
 DB 2220 ATCTTTGGTGAATCTTAGCAAAATTTCAACAAATTTGCAATTTGAGCTAGCAAAATGTT 2279
 QY 2231 CCAGTACATGACCTTAAAGGAGTACTCTTCTTTTACAGGATTTACAGTGAAGTGGC 2290
 DB 2280 CCAGTACATGACCTTAAAGGAGTACTCTTCTTTTACAGGATTTACAGTGAAGTGGC 2339
 QY 2291 TTCACTCTCAGACCTTTATTTTGTGTTGAGTACTCTGTTTGACATTTTGTGTTTGTG 2350
 DB 2340 TTCACTCTCAGACCTTTATTTTGTGTTGAGTACTCTGTTTGACATTTTGTGTTTGTG 2399
 QY 2351 CACTGTGATCTCTGGGAGGGTAGTCTTTTGTCTTCAAGTAAAGTACTTTTACTGACATTT 2410
 DB 2400 CACTGTGATCTCTGGGAGGGTAGTCTTTTGTCTTCAAGTAAAGTACTTTTACTGACATTT 2459
 QY 2411 TCTTCTGGAACAAATACATGCTCTAAGCATTTGTTCTGTTGTTGTTGTTGTTGTTGTTG 2470
 DB 2460 TCTTCTGGAACAAATACATGCTCTAAGCATTTGTTCTGTTGTTGTTGTTGTTGTTGTTG 2519
 QY 2471 GTCAATTTTGTGAATCAAAATACCTTTCCCTTTGTTGTTGTTGTTGTTGTTGTTGTTG 2530
 DB 2520 GTCAATTTTGTGAATCAAAATACCTTTCCCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 2579
 QY 2531 TATGAAGAAATATTTTAGCTGAGTACTATATATTTTACAAATCTTAAAGAAATTTCAAGTT 2590
 DB 2580 TATGAAGAAATATTTTAGCTGAGTACTATATATTTTACAAATCTTAAAGAAATTTCAAGTT 2639
 QY 2591 GGAACCAAGAAATAGCAAGGAAATGTACAAATTTTATCTTCTGCAAGGACATCAT 2650
 DB 2640 GGAACCAAGAAATA---GCAAGGAAATGTACAAATTTTATCTTCTGCAAGGACATCAT 2696
 QY 2651 TCCTGTATTATAGTGTATGTAAATGCACCTGTAAATGTTACTTTGGATTAAATATGGGA 2710
 DB 2697 TCCTGTATTATAGTGTATGTAAATGCACCTGTAAATGTTACTTTCCATTAAATATGGGA 2756
 QY 2711 GGGGGGACTCAAAATTTTCAAGAAAGCTTAAAAA 2746
 DB 2757 -GGGGGACTCAAAATTTTCAAGAAAGCTTAAAAA 2791

RESULT 4

AA154214
 ID AAL54214 standard; DNA; 3702 BP.
 XX
 AC AAL54214;
 XX
 DT 27-MAR-2003 (first entry)
 XX
 DE SR protein-specific kinase-1 DNA, SEQ ID No 6.
 XX
 KW Cytostatic; p53 pathway-modulating agent; SR protein; cancer; apoptosis;
 KW lung cancer; breast cancer; serine/arginine protein-specific kinase;
 KW colon cancer; ovarian cancer; SRPK; cell proliferation; human; ds.
 XX
 OS Homo sapiens.

PN WO200299427-A1.
 XX 12-DEC-2002.
 XX 03-JUN-2002; 2002WO-US017525.
 PF 05-JUN-2001; 2001US-0296076P.
 PR 10-OCT-2001; 2001US-0328605P.
 PR 15-FEB-2002; 2002US-0357253P.
 XX (EXEL-) EXELIXIS INC.
 XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
 XX WPI; 2003-156865/15.
 XX Identifying candidate p53 pathway-modulating agents useful as therapeutic
 targets for disorders related with defective p53 function, by screening
 for agents modulating serine/arginine protein-specific kinase activity.
 XX Disclosure; Page 109-111; 137pp; English.
 XX The invention relates to a novel method for identifying candidate p53
 pathway-modulating agents. The novel method comprises screening for
 agents that modulate the activity of a serine/arginine protein-specific
 kinase. The invention provides methods for utilizing p53 modifier genes
 and polypeptides to identify candidate therapeutic agents that can be
 used in the treatment of disorders associated with defective p53
 function. The methods are also useful for modulating a p53 pathway in a
 mammalian cell, or for diagnosing or treating a disease associated with
 defective p53 function, e.g. cancers such as breast cancer, colon cancer,
 lung cancer or ovarian cancer. The serine/arginine protein-specific
 kinase (SRPK) polypeptides and nucleic acids are useful for identifying
 and testing agents that modulate SRPK function. The animal models are
 useful for in vivo assays to test the activity of a candidate p53-
 modulating agent, or to assess the role of SRPK in a p53 pathway process
 such as apoptosis or cell proliferation. This polynucleotide sequence
 represents the DNA of a serine/arginine-rich domain protein-specific
 kinase-1 of the invention
 XX
 SQ Sequence 3702 BP; 1130 A; 716 C; 823 G; 1033 T; 0 U; 0 Other;
 Query Match 77.9%; Score 2533.8; DB 8; Length 3702;
 Best Local Similarity 99.2%; Pred. No. 0;
 Matches 2568; Conservative 0; Mismatches 17; Indels 4; Gaps 2;
 QY 153 TCCGAAAAAGCCGAGCCTCAACAGAAAGCTCTTTAGTTCTCTCTCCACCGCCACC 212
 DB 202 TTTCAAGAAAGCCGAGCCTCAACAGAAAGCTCTTTAGTTCTCTCTCCACCGCCACC 261
 QY 213 ACCACACACCGCCACCTTTTCCAGACCCACACCCCGAGCCAGAGAGAGATCCT 272
 DB 262 ACCACACACCGCCACCTTTTCCAGACCCACACCCCGAGCCAGAGAGAGATCCT 321
 QY 273 GGGATCAGATGATGAGGAGCAGAGAGCCCTGGGACTACTGCAAGGTTGGATATCATCC 332
 DB 322 GGGATCAGATGATGAGGAGCAGAGAGCCCTGGGACTACTGCAAGGTTGGATATCATCC 381
 QY 333 AGTGAAAAATTTGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 392
 DB 382 AGTGAAAAATTTGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 441
 QY 393 GCATTTCTCTACTGTCTGGCTGTGTTGGATATGACAGGGGAAAAGATTTTGTTCATGAA 452
 DB 442 GCATTTCTCTACTGTCTGGCTGTGTTGGATATGACAGGGGAAAAGATTTTGTTCATGAA 501
 QY 453 AGTTGTTAAAAAGTGGCCAGCATTATACGAGACAGCCTTGGATGAATAAATTTGCTCAA 512
 DB 502 AGTTGTTAAAAAGTGGCCAGCATTATACGAGACAGCCTTGGATGAATAAATTTGCTCAA 561
 QY 513 ATGTGTTTCGAGAAAGTATCCAGTGACCCAAACAAAGACATGGTGGTCACTCATTTGA 572
 DB 562 ATGTGTTTCGAGAAAGTATCCAGTGACCCAAACAAAGACATGGTGGTCACTCATTTGA 621

573	QY	CGACTTCAAGATTTTCAGGCGATGAATGGGATACATGTCTGCAATGTGCTTCGAACTAGCTTGG	632
622	Db	CGACTTCAAGATTTTCAGGCGATGAATGGGATACATGTCTGCAATGTGCTTCGAACTAGCTTGG	681
633	QY	CCACCATCTCTTCAGTGGATCATCAAAATCCAACTATCAAGGCCTCCCAAGTACCTTGTGT	692
682	Db	CCACCATCTCTTCAGTGGATCATCAAAATCCAACTATCAAGGCCTCCCAAGTACCTTGTGT	741
693	QY	GAAGAGTATCATTCGACAGGTCCTTCAAGGGTTAGATTCTTTACACAGTAAGTGCAGAT	752
742	Db	GAAGAGTATCATTCGACAGGTCCTTCAAGGGTTAGATTCTTTACACAGTAAGTGCAGAT	801
753	QY	CATTCTATCTGACATAAAGCCGGAAATATCTTGATGTGTGGAGATGATCATATGTGAG	812
802	Db	CATTCTATCTGACATAAAGCCGGAAATATCTTGATGTGTGGAGATGATCATATGTGAG	861
813	QY	AAGAAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTTCCTTCAGGGTC	872
862	Db	AAGAAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTTCCTTCAGGGTC	921
873	QY	TGCAGTGAAGTACCGGCTCCACAGCAGAAACCTTATAGAAATAATCTTAAACCAAAAGAA	932
922	Db	TGCAGTGAAGTACCGGCTCCACAGCAGAAACCTTATAGAAATAATCTTAAACCAAAAGAA	981
933	QY	AAAACTGAAAGAAAGAAACAGAAAGCAGGCTGAGTTATTTGGAGAAAGCGCTTCAGAGAT	992
982	Db	AAAACTGAAAGAAAGAAACAGAAAGCAGGCTGAGTTATTTGGAGAAAGCGCTTCAGAGAT	1041
993	QY	AGAAAGATTTGGAGCGAGAGCTGAAAGGAAATAATAGAGAAACATCACCTCAGCTGC	1052
1042	Db	AGAAAGATTTGGAGCGAGAGCTGAAAGGAAATAATAGAGAAACATCACCTCAGCTGC	1101
1053	QY	ACCTTCCAATGACCGAGATGCGGAATACTGCCCAGAGGTGAAACTAAAAACAACAGGATT	1112
1102	Db	ACCTTCCAATGACCGAGATGCGGAATACTGCCCAGAGGTGAAACTAAAAACAACAGGATT	1161
1113	QY	AGAGGAGCGGCTCAGGCGAGAGCTGCAAAAGGACAATGGTGAAGCTGAGGACAGGAAGA	1172
1162	Db	AGAGGAGCGGCTCAGGCGAGAGCTGCAAAAGGACAATGGTGAAGCTGAGGACAGGAAGA	1221
1173	QY	GAAGAAGATCTCAGAAAGAAACATTTGAAAGATGAAGATGATGTAGATCAGGAAT	1232
1222	Db	GAAGAAGATCTCAGAAAGAAACATTTGAAAGATGAAGATGATGTAGATCAGGAAT	1281
1233	QY	TGCGAAATAGACCTCAGTGGATAGAAATCACCTTAAACCAATGGCCATTTGAGAAATGG	1292
1282	Db	TGCGAAATAGACCTCAGTGGATAGAAATCACCTTAAACCAATGGCCATTTGAGAAATGG	1341
1293	QY	CCCATTTCTCAGTGGAGCAGCAACTGAGCAGATGAAGATGATGATGAAGACATGCCCCAA	1352
1342	Db	CCCATTTCTCAGTGGAGCAGCAACTGAGCAGATGAAGATGATGATGAAGACATGCCCCAA	1401
1353	QY	TCCTCAGGAATATATCTTGTATGAGCCAAATGCGAGAAAGTGAATACATATAGCAGCTC	1412
1402	Db	TCCTCAGGAATATATCTTGTATGAGCCAAATGCGAGAAAGTGAATACATATAGCAGCTC	1461
1413	QY	CTATGAACAAATTCATTTGATTTGCCAAATTGGACGACATAAATTCGAGTTCACAGATT	1472
1462	Db	CTATGAACAAATTCATTTGATTTGCCAAATTGGACGACATAAATTCGAGTTCACAGATT	1521
1473	QY	CCGAGATTTTCCAGCTCGTTGTTCTCTGGAATCCTTAGAACCTGTGGCTTCGGCTCTGT	1532
1522	Db	CCGAGATTTTCCAGCTCGTTGTTCTCTGGAATCCTTAGAACCTGTGGCTTCGGCTCTGT	1581
1533	QY	GCCTTTCTGAGGGATCACCATTTACTGAGCAAGAGAGAGCAGTCCATCCCATGACAGAG	1592
1582	Db	GCCTTTCTGAGGGATCACCATTTACTGAGCAAGAGAGAGCAGTCCATCCCATGACAGAG	1641
1593	QY	CAGAACGGTTTCAGCCTTCAGTACTGGGATTTGCCAAAGACAAACACCCGGCAGCTGA	1652
1642	Db	CAGAACGGTTTCAGCCTTCAGTACTGGGATTTGCCAAAGACAAACACCCGGCAGCTGA	1701

Qy	1653	CTTTGTTGGTGAATCCCTCGATCCGGGAATGCAGATAAAATTAGCTAATAAAATTCCTGA	1712
Db	1702	CTTTGTTGGTGAATCCCTCGATCCGGGAATGCAGATAAAATTAGCTAATAAAATTCCTGA	1761
Qy	1713	CTTGGGAAATGCTTTGTTGGTGCATAAAACACTTCACGGAAGACATCCAGACGCCTCAGTA	1772
Db	1762	CTTGGGAAATGCTTTGTTGGTGCATAAAACACTTCACGGAAGACATCCAGACGCCTCAGTA	1821
Qy	1773	CCGCTCCATAGAGGTTTTAATAGGAGCGGGGTACAGCACCCCTGGGACATCTGGAGCAC	1832
Db	1822	CCGCTCCATAGAGGTTTTAATAGGAGCGGGGTACAGCACCCCTGGGACATCTGGAGCAC	1891
Qy	1833	GGCGTGATGGCAATTTGAGCTGGCAACGGGAGATTATTTGTTTGAACACACATTTCTGGGA	1892
Db	1882	GGCGTGATGGCAATTTGAGCTGGCAACGGGAGATTATTTGTTTGAACACACATTTCTGGGA	1941
Qy	1893	AGACTATTTCCAGAGACGAAGACCACATAGCCACATCATAGAGCTGCTAGGCAGTATTTCC	1952
Db	1942	AGACTATTTCCAGAGACGAAGACCACATAGCCACATCATAGAGCTGCTAGGCAGTATTTCC	2001
Qy	1953	AAGGCACCTTTGCTCTATCTCGAAAAATATTTCTCGGGAATTTCTTCAATCCGACAGGAGAACT	2012
Db	2002	AAGGCACCTTTGCTCTATCTCGGGAATTTCTCGGGAATTTCTTCAATCCGACAGGAGAACT	2061
Qy	2013	GGGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGAAAAAGTATGG	2072
Db	2062	GGGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGAAAAAGTATGG	2121
Qy	2073	CTGGCCCCATAGAATGCTGCACAGTTTACAGATTTCTTGATCCCGATGTTAGAAATGGT	2132
Db	2122	CTGGCCCCATAGAATGCTGCACAGTTTACAGATTTCTTGATCCCGATGTTAGAAATGGT	2181
Qy	2133	TCAGAAAAACGAGCCTCAGCTGCGGAATGCCCTTCGGCATCTCTTGTTGAAATCTTAGCA	2192
Db	2182	TCAGAAAAACGAGCCTCAGCTGCGGAATGCCCTTCGGCATCTCTTGTTGAAATCTTAGCA	2241
Qy	2193	AAATCTACCAATATTTGCAATCTGAGCTAGCAAAATGTTTCCAGTACATTTGGAACCTAAACGG	2252
Db	2242	AAATCTACCAATATTTGCAATCTGAGCTAGCAAAATGTTTCCAGTACATTTGGAACCTAAACGG	2301
Qy	2253	TGACTCTCAATCTTTTAAACAGATTTACAAGTGAAGTGGCTTCATCCTCAGACCTTTATTTT	2312
Db	2302	TGACTCTCAATCTTTTAAACAGATTTACAAGTGAAGTGGCTTCATCCTCAGACCTTTATTTT	2361
Qy	2313	GCCTTTGAGGTACTGTTGTTTGACATTTTGCTTTTTTGTGCACTGTGATCCTGGGGAAGGCT	2372
Db	2362	GCCTTTGAGGTACTGTTGTTTGACATTTTGCTTTTTTGTGCACTGTGATCCTGGGGAAGGCT	2421
Qy	2373	AGTCTTTTGTCTTTGAGCTTAAGTGTGTTTACTGACCAATTTCTTTCTGGAACCAATAACATGT	2432
Db	2422	AGTCTTTTGTCTTTGAGCTTAAGTGTGTTTACTGACCAATTTCTTTCTGGAACCAATAACATGT	2481
Qy	2433	CTCTAAGCAATCTGTTCTTTGTTGTGTGACATTCAAATGTCAATTTTTTGTGAAATGAAAAAT	2492
Db	2482	CTCTAAGCAATCTGTTCTTTGTTGTGTGACATTCAAATGTCAATTTTTTGTGAAATGAAAAAT	2541
Qy	2493	ACTTTCCCTTTGTGTTTTGGCAGTTTTTGTAACTATTATTAAGAAGAAATATTTTAGCTGA	2552
Db	2542	ACTTTCCCTTTGTGTTTTGGCAGTTTTTGTAACTATTATTAAGAAGAAATATTTTAGCTGA	2601
Qy	2553	GTACTATATAATTTTCAAACTTTAAGAAATTTATCAAGTTTGGGAACCAAGAAATAGCAAGG	2612
Db	2602	GTACTATATAATTTTCAAACTTTAAGAAATTTATCAAGTTTGGGAACCAAGAAATAGCAAGG	2658
Qy	2613	GAATGTACAAATTTTATCTTTCTGGGAAGGGAACATTCATCTGTATTTATAGTGATGTGAA	2672
Db	2659	GAATGTACAAATTTTATCTTTCTGGGAAGGGAACATTCATCTGTATTTATAGTGATGTGAA	2718
Qy	2673	ATGCACCCCTGTAATGTTACTTTTGGATTAATAATATGGGAGGGGGGCACTCAAAATTTTCAGAAA	2732
Db	2719	ATGCACCCCTGTAATGTTACTTTTCCATTAATAATATGGGA - GGGGGACTCAAAATTTTCAGAAA	2777
Qy	2733	AGCTAAAAA 2741	


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Db      2778 AGTACCAA 2786
|||||
RESULT 5
ADJ96579
ID      ADJ96579 standard; DNA; 3715 BP.
XX      AC
XX      ADJ96579;
XX      DT
XX      06-MAY-2004 (first entry)
XX      DE
XX      Human SRPK2 DNA SeqID 36.
XX      gene; ds; kinase; human; SNP; single nucleotide polymorphism;
KW      tyrosine protein kinase; serine/threonine protein kinase; PK; STK;
KW      gene therapy; cancer; immune-related disease; cardiovascular disease;
KW      brain; neuronal associated disease; metabolic; inflammatory disorder;
KW      cystostatic; neuroprotective; immunomodulator; antiinflammatory; SRPK2.
XX      OS
XX      Homo sapiens.
XX      24.
XX      FH
XX      Key      Location/Qualifiers
FT      variation replace(1969,t)
FT      /tag= a
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation replace(1996,g)
FT      /tag= b
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation replace(1999,g)
FT      /tag= c
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation replace(2001,a)
FT      /tag= d
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation replace(2014,a)
FT      /tag= e
FT      /standard_name= "Single nucleotide polymorphism"
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FT      /tag= f
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation replace(2017,c)
FT      /tag= g
FT      /standard_name= "Single nucleotide polymorphism"
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FT      /standard_name= "Single nucleotide polymorphism"
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FT      /tag= j
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FT      /standard_name= "Single nucleotide polymorphism"
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FT      /tag= n
FT      /standard_name= "Single nucleotide polymorphism"
FT      variation replace(2219,t)
FT      /tag= o
FT      /standard_name= "Single nucleotide polymorphism"
XX      PN
XX      WO2004006838-A2.
XX      22-JAN-2004.

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XX      15-JUL-2003; 2003WO-US021730.
XX      PF
XX      PR      15-JUL-2002; 2002US-0395632P.
XX      PA
XX      (SUGB-) SUGEN INC.
XX      PI
XX      Whyte D, Manning G, Caenepeel S;
XX      WPI; 2004-122753/12.
XX      DR      P-PSDB; ADJ96645.
XX      PT
XX      New nucleic acid molecule encoding a kinase polypeptide, useful for
XX      preparing a composition for treating diseases or disorders, e.g., cancer,
XX      or neurological, immunological or inflammatory disorders.
XX      PS
XX      Example 1; SEQ ID NO 36; 365pp; English.
XX      CC
XX      This invention relates to a novel isolated, enriched or purified nucleic
XX      acid molecule that encodes a kinase polypeptide. Specifically, it relates
XX      to human tyrosine and serine/threonine protein kinases (PK's and STK's),
XX      as well as protein kinase-like enzymes. The present invention describes
XX      screening methods to identify agonists, antagonists and antibodies that
XX      can be used to modulate the activity or function of the mammalian kinase
XX      enzymes. As such, these compositions can be used for gene therapy
XX      purposes to treat diseases or disorders including cancer, immune-related
XX      diseases, cardiovascular disease, brain or neuronal associated disease,
XX      metabolic and inflammatory disorders. Accordingly, they exhibit
XX      cytostatic, neuroprotective, immunomodulator and antiinflammatory
XX      activities. This polynucleotide sequence is a human kinase DNA sequence
XX      of the invention.
XX      SQ      Sequence 3715 BP; 1135 A; 719 C; 825 G; 1036 T; 0 U; 0 Other;
XX
XX      Query Match      77.9%; Score 2533.8; DB 12; Length 3715;
XX      Best Local Similarity 99.2%; Pred. No. 0;
XX      Matches 2568; Conservative 0; Mismatches 17; Indels 4; Gaps 2;
XX
QY      153 TCCGAAAAGCCGAGACCTTCAACAGAAAGCTCCTTAGTTCCTCTCCACCGCCACC 212
DB      208 TTGAGAAAGCCGAGACCTTCAACAGAAAGCTCCTTAGTTCCTCTCCACCGCCACC 267
QY      213 ACCACACACCCGAGACCTTTCGAGACCCACACCCCGGAGCCAGAGAGAGATCCT 272
DB      268 ACCACACACCCGAGACCTTTCGAGACCCACACCCCGGAGCCAGAGAGAGATCCT 327
QY      273 GGGATCAGATGATGAGGAGCAGACCTTCGGGACTACTGCAAGAGTGGATATCATCC 332
DB      328 GGGATCAGATGATGAGGAGCAGAGGACCTTCGGGACTACTGCAAGAGTGGATATCATCC 387
QY      333 AGTGAATAATGGAGACCTTTCGAGGCGGATATCATGTTATAGAAAGCTGGATGGGG 392
DB      388 AGTGAATAATGGAGACCTTTCGAGGCGGATATCATGTTATAGAAAGCTGGATGGGG 447
QY      393 GCACCTTCTACTGCTGCTGGGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 452
DB      448 GCACCTTCTACTGCTGCTGGGATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 507
QY      453 AGTTGTAATAAGTGCAGCATTATACGGAGAGCAGCCTTGGGATGAATAAATTTGCTCAA 512
DB      508 AGTTGTAATAAGTGCAGCATTATACGGAGAGCAGCCTTGGGATGAATAAATTTGCTCAA 567
QY      513 ATGTGTTTCGAGAAAGTATCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATTTGA 572
DB      568 ATGTGTTTCGAGAAAGTATCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATTTGA 627
QY      573 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTCTGATGGTCTTTCGAAGTACTTGG 632
DB      628 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTCTGATGGTCTTTCGAAGTACTTGG 687
QY      633 CCACCATCTCCTCAAGTGGATCATCAAAATCCAACTATCAAGGCTCCAGTACGTTGTGT 692
DB      688 CCACCATCTCCTCAAGTGGATCATCAAAATCCAACTATCAAGGCTCCAGTACGTTGTGT 747

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693	QY	GAAGAGTATCATTTGACAGAGTCTTTCAAGGGTTAGATTACTTACACAGTAGTGCACAGAT	752
748	Db	GAAGAGTATCATTTGACAGAGTCTTTCAAGGGTTAGATTACTTACACAGTAGTGCACAGAT	807
753	QY	CATTTCATCTGACATAAAGCCGGAAATATCTTGATGTGTGATGTGATGATGATATGTGAG	812
808	Db	CATTTCATCTGACATAAAGCCGGAAATATCTTGATGTGTGATGTGATGATGATATGTGAG	867
813	QY	AAGAAATGGCAGCTGAGGCCACTTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCAGGGTC	872
868	Db	AAGAAATGGCAGCTGAGGCCACTTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCAGGGTC	927
873	QY	TGCAGTGAGTAGCGGTCTCACAGCAAAACCTTAGAAGAAATATCTAAGAAACAAAAAGAA	932
928	Db	TGCAGTGAGTAGCGGTCTCACAGCAAAACCTTAGAAGAAATATCTAAGAAACAAAAAGAA	987
933	QY	AAAACTGAAAAAGAAACAGAGAGCGAGGCTCAGTTATTGGAGAAAGCCCTGCAGGAGAT	992
988	Db	AAAACTGAAAAAGAAACAGAGAGCGAGGCTCAGTTATTGGAGAAAGCCCTGCAGGAGAT	1047
993	QY	AGAAGAATTTGGACGCGAAGAGCTGAAAGGAAATATATAGAGAAACATCATCCTCAGCTGC	1052
1048	Db	AGAAGAATTTGGACGCGAAGAGCTGAAAGGAAATATATAGAGAAACATCATCCTCAGCTGC	1107
1053	QY	ACCTTCCAAATGACCAGATGGCGAATACCTGCCAGAGGTGAAATCTAAAAACAAACAGGATT	1112
1108	Db	ACCTTCCAAATGACCAGATGGCGAATACCTGCCAGAGGTGAAATCTAAAAACAAACAGGATT	1167
1113	QY	AGAGGAGGGCGCTGAGGCGAGAGCTCCAAAGGACAAATGTTGAAGCTGAGGACACAGAGAGA	1172
1168	Db	AGAGGAGGGCGCTGAGGCGAGAGCTCCAAAGGACAAATGTTGAAGCTGAGGACACAGAGAGA	1227
1173	QY	GAAGAAGATGCTGAGAAAGAAACAACTGAAAGAGATGAAGATGATGTAGATCAGGAAT	1232
1228	Db	GAAGAAGATGCTGAGAAAGAAACAACTGAAAGAGATGAAGATGATGTAGATCAGGAAT	1287
1233	QY	TGCGAACATAGACCCCTACGTGGTAGAATCACCTAAAAACCAATGGCCATATTGAGAAATGG	1292
1288	Db	TGCGAACATAGACCCCTACGTGGTAGAATCACCTAAAAACCAATGGCCATATTGAGAAATGG	1347
1293	QY	CCCATTTCTGAGAGCAGCAACTGACGAGTGAAGATGATGAAGAAAGACTGCCCCAAA	1352
1348	Db	CCCATTTCTGAGAGCAGCAACTGCGACGATGAAGATGATGAAGAAAGACTGCCCCAAA	1407
1353	QY	TCCTTGAGGAATATAATCTTGATGAGCCAAAATGAGAAAGTGATTACACATATAGCAGCTC	1412
1408	Db	TCCTTGAGGAATATAATCTTGATGAGCCAAAATGAGAAAGTGATTACACATATAGCAGCTC	1467
1413	QY	CTATGAAACAATTCATGAGTGAATTCGCAATGGACGACATAAATTTCCGAGTGCAGATT	1472
1468	Db	CTATGAAACAATTCATGAGTGAATTTGCCAAAATGGACGACATAAATTTCCGAGTGCAGATT	1527
1473	QY	CCGAGATTTTCCACCTCTGTTTCTCTGGAATCCTTAGAACCTGTGGCCCTGCGGCTCTGT	1532
1528	Db	CCGAGATTTTCCACCTCTGTTTCTCTGGAATCCTTAGAACCTGTGGCCCTGCGGCTCTGT	1587
1533	QY	GCTTTCTGAGGGATCACACATTAATGACAGAGGAGAGCAGTCCATCCATGACAGAG	1592
1598	Db	GCTTTCTGAGGGATCACACATTAATGACAGAGGAGAGCAGTCCATCCATGACAGAG	1647
1593	QY	CAGAACGTTTTACGCTCCAGTCTGGGGATTTGCCAAAAGCAAAAAACCCGGGACGCTGA	1652
1648	Db	CAGAACGTTTTACGCTCCAGTCTGGGGATTTGCCAAAAGCAAAAAACCCGGGACGCTGA	1707
1653	QY	CTTGTGTGTGAATCCCTCTGGATCCGCGGAATGCAGATATAAATTAGAGTAAAAATTGCTGA	1712
1708	Db	CTTGTGTGTGAATCCCTCTGGATCCGCGGAATGCAGATATAAATTAGAGTAAAAATTGCTGA	1767
1713	QY	CCTGGGAAATGCTGTTGGTGCATAAACATCTCACGGAAGACATCCAGACCGCTCAGTA	1772
1768	Db	CCTGGGAAATGCTGTTGGTGCATAAACATCTCACGGAAGACATCCAGACCGCTCAGTA	1827

RESULT 6
ABK51173
ID ABK51173 standard; cDNA; 3745 BP.
XX

AC ABK51173;
XX 30-JUL-2002 (first entry)
DT cDNA encoding human cellular kinase SRPK-2 protein.
XX
DE Human; virucide; cytomegalovirus infection; CMV; cellular kinase; RICK;
KW RIP; Nck-Interacting kinase; MKK3; SRPK-2; gene; ss.
KW
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH 188..2248
FT CDS
FT /*tag= a
FT /product= "Human cellular kinase SRPK-2"
XX
XX EP1201765-A2.
XX
XX 02-MAY-2002.
XX
XX 15-OCT-2001; 2001EP-00124604.
XX
XX 16-OCT-2000; 2000US-0240750P.
XX
XX (AXXI-) AXIMA PHARM AG.
XX
XX Schubart D, Habenberger P, Stein-Gerlach M, Bevec D;
PI
XX WPI; 2002-373930/41.
XX P-PSDB; AAU80373.
XX
XX Identifying agents for treatment or prevention of cytomegalovirus
PT infection, comprises contacting test compound with cellular kinase and
PT detecting change in cellular kinase activity.
XX
XX Disclosure; Page 39-43; 49pp; English.
XX
XX The present invention relates to a new method for identifying compounds
CC for treating and/or preventing cytomegalovirus (CMV) infection and/or
CC related diseases. The method of the invention comprises contacting a test
CC compound with at least one of the cellular kinases RICK, RIP, Nck-
CC Interacting kinase, MKK3 and SRPK-2 and detecting any change in kinase
CC activity. The method of the invention can be used to treat and/or prevent
CC CMV infections and related diseases. Oligonucleotides that can detect the
CC specified kinases can also be used for diagnosis of infection. The
CC present nucleic acid sequence encodes the human cellular kinase SRPK-2
CC protein of the invention, as described above
XX
XX Sequence 3745 BP; 1163 A; 719 C; 829 G; 1034 T; 0 U; 0 Other;
SQ
Query Match 76.8%; Score 2497; DB 6; Length 3745;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2559; Conservative 0; Mismatches 20; Indels 10; Gaps 4;
QY 153 TCGAAGGCGGAGCCTCAACAGAAAGCTCTTCTAGTTCCTCTCTCCACCGCCACC 212
DB 217 TTCAGAAAGCGCGGAGCCTCAACAGAAAGCTCTTCTAGTTCCTCTCTCCACCGCCACC 276
QY 213 ACCACACACCCACCTTTGCGAGACCCACACCCCGGAGCCAGAGGAGGATCCT 272
DB 277 ACCACACACCCACCTTTGCGAGACCCACACCCCGGAGCCAGAGGAGGATCCT 336
QY 273 GGGATCAGATGATGAGGAGCAAGAGACCTCGGACTACTGCAAGGTGGATATCATCC 332
DB 337 GGGATCAGATGATGAGGAGCAAGAGACCTCGGACTACTGCAAGGTGGATATCATCC 396
QY 333 AGTGAAGATTGAGACCTCTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 392
DB 397 AGTGAAGATTGAGACCTCTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 456
QY 393 GCACCTTCTACTGTCTGCTGTGGATATGACAGGGGAAAGATTGTTGCAATGAA 452
DB 457 GCACCTTCTACTGTCTGCTGTGGATATGACAGGGGAAAGATTGTTGCAATGAA 516

QY 453 AGTTGTTAAAGTGTCCAGCATTTATACGGAGACAGCCTTGGATGAATAAATTTGCTCAA 512
DB 517 AGTTGTTAAAGTGTCCAGCATTTATACGGAGACAGCCTTGGATGAATAAATTTGCTCAA 576
QY 513 ATGTGTTTCGAGAAAGTGTCCAGTGCACCAACAAAGACATGGTGGTCCAGCTCATTTGA 572
DB 577 ATGTGTTTCGAGAAAGTGTCCAGTGCACCAACAAAGACATGGTGGTCCAGCTCATTTGA 636
QY 573 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGTCATGGTCTTCGAAGTACTTGG 632
DB 637 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGTCATGGTCTTCGAAGTACTTGG 696
QY 633 CCACCATCTCTCAAGTGGATCATCAAAATCCAAGTATCAAGGCCTCCAGTACGTTGTGT 692
DB 697 CCACCATCTCTCAAGTGGATCATCAAAATCCAAGTATCAAGGCCTCCAGTACGTTGTGT 756
QY 693 GAAAGAGTATCATTCGACAGGTCTCTCAAGGGTTAGATTACTTACACAGTAAGTGAAGAT 752
DB 757 GAAAGAGTATCATTCGACAGGTCTCTCAAGGGTTAGATTACTTACACAGTAAGTGAAGAT 816
QY 753 CATTCATCTGACATATAAGCCGGAATAATCTTGTATGTGTGGATGATGCATATGTGAG 812
DB 817 CATTCATCTGACATATAAGCCGGAATAATCTTGTATGTGTGGATGATGCATATGTGAG 876
QY 813 AAGAATGGCAGCTGAGGCCAATGAGTGGCAGAAAGCAGGTCTCTCTCTCTTCAGGGTC 872
DB 877 AAGAATGGCAGCTGAGGCCAATGAGTGGCAGAAAGCAGGTCTCTCTCTCTTCAGGGTC 933
QY 873 TGCAGTGTAGTACGGCTCCACAGCAGAAACCTTATAGGAAAAATATCTAAAAACAAAAAGAA 932
DB 934 TGCAGTGTAGTACGGCTCCACAGCAGAAACCTTATAGGAAAAATATCTAAAAACAAAAAGAA 993
QY 933 AAAAAGTGAAGAAAGAAAGCAGGAGCAGGTCTGAGTATTTGGAGAGCGCTGTCAGGAGAT 992
DB 994 AAAAAGTGAAGAAAGAAAGCAGGAGCAGGTCTGAGTATTTGGAGAGCGCTGTCAGGAGAT 1053
QY 993 AGAAGAAATTTGAGCGAGAAAGCTGAAAGGAAATATATAGAGAAAAACATCACCTCAGCTGC 1052
DB 1054 AGAAGAAATTTGAGCGAGAGAGCTGAAAGGAAATATATAGAGAAAAACATCACCTCAGCTGC 1113
QY 1053 ACCTTCCATATGACAGGAGTGGCGAATATCTGCCAGAGGTGAACTAAAAACACAGGAT 1112
DB 1114 ACCTTCCATATGACAGGAGTGGCGAATATCTGCCAGAGGTGAACTAAAAACACAGGAT 1173
QY 1113 AGAGGAGCGGTGAGGAGCAGACACTGCAAGAGCAATGTGAAGCTGAGGACACAGGAAGA 1172
DB 1174 AGAGGAGCGGTGAGGAGCAGACACTGCAAGAGCAATGTGAAGCTGAGGACACAGGAAGA 1233
QY 1173 GAAAGAAATGCTGAGAAAGAAAAATTGAAAAAGATGAAGATGATGTAGATCAGGAAT 1232
DB 1234 GAAAGAAATGCTGAGAAAGAAAAATTGAAAAAGATGAAGATGATGTAGATCAGGAAT 1293
QY 1233 TCGCAACATAGACCTTACGTGGATAGAAATCCTTAAACCAATGGCCATATTGAGATGG 1292
DB 1294 TCGCAACATAGACCTTACGTGGATAGAAATCCTTAAACCAATGGCCATATTGAGATGG 1353
QY 1293 CCATTTCTCCTGAGCAGCAACTGAGCAGATGAAGATGATGAAGAGACTGCCCAAA 1352
DB 1354 CCATTTCTCCTGAGCAGCAACTGAGCAGATGAAGATGATGAAGAGACTGCCCAAA 1413
QY 1353 TCCTGAGGAATATAATCTTGTATGAGCCAAATCGAAAAAGTGAATACATATAGCAGCTC 1412
DB 1414 TCCTGAGGAATATAATCTTGTATGAGCCAAATCGAAAAAGTGAATACATATAGCAGCTC 1473
QY 1413 CTATGAACAAATTCATGTTGATGAGCCAAATCGAAAAAGTGAATACATATAGCAGCTC 1472
DB 1474 CTATGAACAAATTCATGTTGATGAGCCAAATCGAAAAAGTGAATACATATAGCAGCTC 1533
QY 1473 CCAGAGTTTTCACCTCGTTGTTCTCTGGATCTCTTAGAACCTGTGGCTGGGGCTCTGT 1532
DB 1534 CCAGAGTTTTCACCTCGTTGTTCTCTGGATCTCTTAGAACCTGTGGCTGGGGCTCTGT 1593

CC hyperproliferating skin diseases, psoriasis, diabetes mellitus Type I
CC and/or II. Sequences of the invention are also useful as inhibitors for
CC mycobacterial protein kinases, nuclear export of TNF-alpha mRNA in TNF-
CC alpha mediated diseases, protein kinase and/or phosphatase and cellular
CC hyperproliferation of cancer cells. The invention is useful for treating
CC opportunistic infections (e.g. cancer, mycobacteria-induced opportunistic
CC infections), diabetes, inflammation, cancer cachexia, necrosis, gastric
CC ulcers, influenza multiple sclerosis, neuropathic diseases, neuropathic
CC pain and polynuropathy, neurodegenerative diseases (Alzheimer's disease,
CC Parkinson's disease), neurological disorder, gastrointestinal ulcerative,
CC Huntington's chorea, peripheral and/or central nerve diseases, atopic
CC eczema, psoriasis, urticaria, allergic reactions, rheumatoid arthritis,
CC osteoarthritis, ulcerative colitis, Crohn's disease, ischaemic diseases
CC and ischaemic heart disease, liver diseases and dysfunction of liver,
CC cardiovascular diseases, psychiatric disorders, schizophrenia, stroke,
CC alcoholism, attention deficit disorder, depression, obesity, learning
CC disabilities, pain, senile macular degeneration, diseases affecting the
CC immune system, impotence, male infertility, respiratory disorders, asthma
CC and infections. The present sequence is a human DNA related to the
CC invention
XX
SQ

Sequence 3745 BP; 1163 A; 719 C; 829 G; 1034 T; 0 U; 0 Other;

Query Match 76.8%; Score 2497; DB 8; Length 3745;
Best Local Similarity 98.8%; Pred. No. 0;
Matches 2559; Conservative 0; Mismatches 20; Indels 10; Gaps 4;
QY 153 TCCGAAAAAGCCGAGCCTCAACAGAAAGCTCTTTAGTTCCTCTCCCTCCACCGCCACC 212
DB 217 TTCAGAAAGCCGAGCCTCAACAGAAAGCTCTTTAGTTCCTCTCCCTCCACCGCCACC 276
QY 213 ACCACACACCGCCACCTTTGCCAGACCCACACCCCGGAGCCAGAGAGAGATCCT 272
DB 277 ACCACACACCGCCACCTTTGCCAGACCCACACCCCGGAGCCAGAGAGAGATCCT 336
QY 273 GGGATCAGATGATGAGGACGACGAGGACCTCGGACTACTGCAAGGTGGATATCATCC 332
DB 337 GGGATCAGATGATGAGGACGACGAGGACCTCGGACTACTGCAAGGTGGATATCATCC 396
QY 333 AGTGAAAAATTGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGGG 392
DB 397 AGTGAAAAATTGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGGG 456
QY 393 GCACCTCTCTACTGTCTGCTGTGCTGGATATGCGAGGGGAAAGATTTGTCGAATGAA 452
DB 457 GCACCTCTCTACTGTCTGCTGTGCTGGATATGCGAGGGGAAAGATTTGTCGAATGAA 516
QY 453 AGTTGTAAGGAGTCCAGCATTATACGGAGACAGCCTTTGGATGAATAAATTTGCTCAA 512
DB 517 AGTTGTAAGGAGTCCAGCATTATACGGAGACAGCCTTTGGATGAATAAATTTGCTCAA 576
QY 513 ATGTGTTTCGAGAAAGTGATCCCAAGTACCCCAACAAAGACATGGTGGTCCAGCTCATGGA 572
DB 577 ATGTGTTTCGAGAAAGTGATCCCAAGTACCCCAACAAAGACATGGTGGTCCAGCTCATGGA 636
QY 573 CGACTTCAAGATTTACGAGCATGAATGGGATACATGTCGATGCTTCCAGAGTACTGG 632
DB 637 CGACTTCAAGATTTACGAGCATGAATGGGATACATGTCGATGCTTCCAGAGTACTGG 696
QY 633 CCACCATCTCTCAAGTGGATCATCAATCCAACTATCAAGGCTCCCAAGTACTGGTGTCT 692
DB 697 CCACCATCTCTCAAGTGGATCATCAATCCAACTATCAAGGCTCCCAAGTACTGGTGTCT 756
QY 693 GAAGAGTATCATTCGACAGGCTCTTCAAGGGTTAGATTTACTTACACAGTAAGTGCAGAT 752
DB 757 GAAGAGTATCATTCGACAGGCTCTTCAAGGGTTAGATTTACTTACACAGTAAGTGCAGAT 816
QY 753 CATTTACTGACATAAAGCCGAAATATCTTTGATGTGTGGATGATGATATGTGAG 812
DB 817 CATTTACTGACATAAAGCCGAAATATCTTTGATGTGTGGATGATGATATGTGAG 876
QY 813 AAGMATGGCAGCTGAGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCAGGTC 872
DB 872 AAGMATGGCAGCTGAGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCAGGTC 932
QY 873 TGCAGTGAAGTACGGTCTCCACAGCAAACTTATAGAAATAATCTTAAACAAAAAGAA 932
DB 934 TGCAGTGAAGTACGGTCTCCACAGCAAACTTATAGAAATAATCTTAAACAAAAAGAA 993
QY 933 AAAAAGTGAAGAAACAGCAAGAGCAGCTGAGTTATTTGGAGAACGCTGTCAGGAGAT 992
DB 994 AAAAAGTGAAGAAACAGCAAGAGCAGCTGAGTTATTTGGAGAACGCTGTCAGGAGAT 1053
QY 993 AGAAGAAATTTGAGCGAGAAAGCTGAAAGGAAAAATAATAGAGAAAAACATCACCTCAGTGC 1052
DB 1054 AGAAGAAATTTGAGCGAGAAAGCTGAAAGGAAAAATAATAGAGAAAAACATCACCTCAGTGC 1113
QY 1053 ACCTTCCAAATGACAGGATGGGGAATACCTCCAGAGGTGAAACTTAAAAACAACAGATTT 1112
DB 1114 ACCTTCCAAATGACAGGATGGGGAATACCTCCAGAGGTGAAACTTAAAAACAACAGATTT 1173
QY 1113 AGAGAGGCGGCTGAGGCGAGAGACTGCAAGAGCAATGTTGAAGCTGAGACCCAGGAAGA 1172
DB 1174 AGAGAGGCGGCTGAGGCGAGAGACTGCAAGAGCAATGTTGAAGCTGAGACCCAGGAAGA 1233
QY 1173 GAAAGAAATGCTGAGAAAGAAAAACATTTGAAAAAGATGAAGATGTTAGATCAGGAAC 1232
DB 1234 GAAAGAAATGCTGAGAAAGAAAAACATTTGAAAAAGATGAAGATGTTAGATCAGGAAC 1293
QY 1233 TCGGAAACATAGACCTTACGTGATAGAAATCACCTTAAACCAATGGCCATATTGAGAAATGG 1292
DB 1294 TCGGAAACATAGACCTTACGTGATAGAAATCACCTTAAACCAATGGCCATATTGAGAAATGG 1353
QY 1293 CCCATCTCAGCTGGAGCAGCAACTGGACGATGAAGATGATGAAGAAAGACTGCCCAAA 1352
DB 1354 CCCATCTCAGCTGGAGCAGCAACTGGACGATGAAGATGATGAAGAAAGACTGCCCAAA 1413
QY 1353 TCTGAGGAATAATCTTGTATGAGCCAAATGCGAAAGATGATACACATATAGCAGCTC 1412
DB 1414 TCTGAGGAATAATCTTGTATGAGCCAAATGCGAAAGATGATACACATATAGCAGCTC 1473
QY 1413 CTATGAACAAATTTCAATGGTGAATTTGCCAAATGGAACATAAAATTTCCGAGTCAAGTT 1472
DB 1474 CTATGAACAAATTTCAATGGTGAATTTGCCAAATGGAACATAAAATTTCCGAGTCAAGTT 1533
QY 1473 CCCAGAGTTTCCACCTGCTTCTCTGGATCTTAGAACCTGCTGGCTGGCTGGCTCTGT 1532
DB 1534 CCCAGAGTTTCCACCTGCTTCTCTGGATCTTAGAACCTGCTGGCTGGCTGGCTCTGT 1593
QY 1533 GCTTCTGAGGATCACCACTTACTGAGCAAGAGGAGAGCAGTCCATCCCATGACAGAAG 1592
DB 1594 GCTTCTGAGGATCACCACTTACTGAGCAAGAGGAGAGAGCAGTCCATCCCATGACAGAAG 1653
QY 1593 CAGAACGGTTTTCAGGCTCCAGTACCTGGGATTTGCCAAAGCAAAACCCGGGCGAGCTGA 1652
DB 1654 CAGAACGGTTTTCAGGCTCCAGTACCTGGGATTTGCCAAAGCAAAACCCGGGCGAGCTGA 1713
QY 1653 CTGTGTTGGTGAATCCCTGGATCCCGGGAATGCGAGATAAATTTAGATGAATAATTTCTGA 1712
DB 1714 CTGTGTTGGTGAATCCCTGGATCCCGGGAATGCGAGATAAATTTAGATGAATAATTTCTGA 1773
QY 1713 CTGTGGAATGCTTGTGTTGGTGCATAAAACACTTTCCGGAAGACATCCAGACGGTCAAGTA 1772
DB 1774 CTGTGGAATGCTTGTGTTGGTGCATAAACAATTTCCGGAAGACATCCAGACGGTCAAGTA 1833
QY 1773 CCGCTCCATAGAGTTTAAATAGGAGCGGGGTACAGCACCCCTCGCGGACATCTGGAGCAC 1832
DB 1834 CCGCTCCATAGAGTTTAAATAGGAGCGGGGTACAGCACCCCTCGCGGACATCTGGAGCAC 1893
QY 1833 GCGGTGATGCGATTTGAGCTGCGCAACCGGAGATTTATTTGTTGAACCAATTTCTGGGA 1892
DB 1894 GCGGTGATGCGATTTGAGCTGCGCAACCGGAGATTTATTTGTTGAACCAATTTCTGGGA 1953
QY 1893 AGACTATTTCCAGAGAGGAAGACACATAGCCACATCATAGAGCTGCTAGGCGAGTATTC 1952
DB 1954 AGACTATTTCCAGAGAGGAAGACACATAGCCACATCATAGAGCTGCTAGGCGAGTATTC 2013

QY	1953	AAGGACATTTGCTCTATCTGGAATAATTTCTCGGAATTTCTTCAATCGAGAGAGAACT	2012	XX	WO200299427-A1.
Db	2014	AAGGACATTTGCTCTATCTGGAATAATTTCTCGGAATTTCTTCAATCGAGAGAGAACT	2073	XX	12-DEC-2002.
QY	2013	GGGACATACCAAGCTGAAGCCCTGAGCCTCTTTGATGTAATTTGGAAGAATGATGG	2072	XX	03-JUN-2002; 2002WO-US017525.
Db	2074	GGGACATACCAAGCTGAAGCCCTGAGCCTCTTTGATGTAATTTGGAAGAATGATGG	2133	XX	05-JUN-2001; 2001US-0296076P.
QY	2073	CTGGCCCATGAAGATGCTGCACAGTTTACAGATTTCTCGATCCCGATGTTAGAAATGGT	2132	XX	10-OCT-2001; 2001US-0328605P.
Db	2134	CTGGCCCATGAAGATGCTGCACAGTTTACAGATTTCTCGATCCCGATGTTAGAAATGGT	2193	XX	15-FEB-2002; 2002US-0357253P.
QY	2133	TCAGAAAAACGAGCCTCAGCTGGGGAATGCCCTCGGCATCCTTGGTTGAATTTCTTAGCA	2192	XX	(EXEL-) EXELIXIS INC.
Db	2194	TCAGAAAAACGAGCCTCAGCTGGGGAATGCCCTCGGCATCCTTGGTTGAATTTCTTAGCA	2250	XX	Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
QY	2193	AATTTACCAATTTGCAATTTCTGAGCTAGCAATGTTCCAGTACATTTGGACCTTAAACGG	2252	XX	WFI; 2003-156865/15.
Db	2251	AATTTACCAATTTGCAATTTCTGAGCTAGCAATGTTCCAGTACATTTGGACCTTAAACGG	2310	XX	Identifying candidate p53 pathway-modulating agents useful as therapeutic
QY	2253	TGACTCTCATTTCTTAAACAGGATTTACAAGTGAAGCTGGCTTCATCTCAGACCTTTATTTT	2312	XX	targets for disorders related with defective p53 function, by screening
Db	2311	TGACTCTCATTTCTTAAACAGGATTTACAAGTGAAGCTGGCTTCATCTCAGACCTTTATTTT	2370	XX	for agents modulating serine/arginine protein-specific kinase activity.
QY	2313	GCCTTGAGGTAAGTTGTTGATGATTTGCTTTTGTGCACTGATCTCTGGGAAGGT	2372	XX	Example; Page 111-113; 137pp; English.
Db	2371	GCCTTGAGGTAAGTTGTTGATGATTTGCTTTTGTGCACTGATCTCTGGGAAGGT	2430	XX	The invention relates to a novel method for identifying candidate p53
QY	2373	AGCTTTTGTCTCAGCTAAGTAGTTTACTGACCAATTTTCTTCTGGAACAATAACATGT	2432	XX	pathway-modulating agents. The novel method comprises screening for
Db	2431	AGCTTTTGTCTCAGCTAAGTAGTTTACTGACCAATTTTCTTCTGGAACAATAACATGT	2490	XX	agents that modulate the activity of a serine/arginine protein-specific
QY	2433	CTCTAAGCAATGTTCTTGTGTTGTGCACTTCAATGATGATTTTGTGAATGAATAT	2492	XX	kinase. The invention provides methods for utilizing p53 modifier genes
Db	2491	CTCTAAGCAATGTTCTTGTGTTGTGCACTTCAATGATGATTTTGTGAATGAATAT	2550	XX	and polypeptides to identify candidate therapeutic agents that can be
QY	2493	ACTTTCCCTTCTGTTTGGCAGGTTTGTGTAATTTATGAGAAATATTTTAGCTGA	2552	XX	used in the treatment of disorders associated with defective p53
Db	2551	ACTTTCCCTTCTGTTTGGCAGGTTTGTGTAATTTATGAGAAATATTTTAGCTGA	2610	XX	function. The methods are also useful for modulating a p53 pathway in a
QY	2553	GTACTATATTAATTTACAATCTTAAGAAATATATCAAGTTGGGAACCAAGAAATAGCAAG	2612	XX	mammalian cell, or for diagnosing or treating a disease associated with
Db	2611	GTACTATATTAATTTACAATCTTAAGAAATATATCAAGTTGGGAACCAAGAAATAGCAAG	2667	XX	defective p53 function, e.g. cancers such as breast cancer, colon cancer,
QY	2613	GAAATGTACAAATTTTATCTTCTGCAAGGACATCATCTCTGATTTATGTTAGTGTAA	2672	XX	lung cancer or ovarian cancer. The serine/arginine protein-specific
Db	2668	GAAATGTACAAATTTTATCTTCTGCAAGGACATCATCTCTGATTTATGTTAGTGTAA	2727	XX	kinase (SRPK) polypeptides and nucleic acids are useful for identifying
QY	2673	ATGCACCTGTAAATGTTTACTTTGGATTAAATATGAGGGGGGAGCTCAAAATTCAGAAA	2732	XX	and testing agents that modulate SRPK function. The animal models are
Db	2728	ATGCACCTGTAAATGTTTACTTTCCATTAATATGGA-GGGGAGCTCAAAATTCAGAAA	2786	XX	useful for in vivo assays to test the activity of a candidate p53-
QY	2733	AGCTAAAAA 2741		XX	modulating agent, or to assess the role of SRPK in a p53 pathway process
Db	2787	AGCTAACCA 2795		XX	such as apoptosis or cell proliferation. This polynucleotide sequence
RESULT 8				XX	represents the DNA of a serine/arginine-rich domain protein-specific
AAL54215				XX	kinase-1 of the invention
XX	AAL54215	standard; DNA; 3745 BP.		XX	SQ Sequence 3745 BP; 1163 A; 719 C; 829 G; 1034 T; 0 U; 0 Other;
AC	AAL54215;			XX	Query Match 76.8%; Score 2497; DB 8; Length 3745;
XX	27-MAR-2003 (first entry)			XX	Best Local Similarity 98.8%; Pred. No. 0;
DT	SR protein-specific kinase-1 DNA, SEQ ID No 7.			XX	Matches 2559; Conservative 0; Mismatches 20; Indels 10; Gaps 4;
DE	Cytostatic; p53 pathway-modulating agent; SR protein; cancer; apoptosis;			XX	QY 153 TCCGAAAAAGCCGAGAGCTTCAACAGAAAGCTCTTTAGTTCTCTCTCCACCGCCACC 212
KW	lung cancer; breast cancer; serine/arginine protein-specific kinase;			XX	217 TTCAGAAAGCCGAGAGCTTCAACAGAAAGCTCTTTAGTTCTCTCTCCACCGCCACC 276
KW	colon cancer; ovarian cancer; SRPK; cell proliferation; human; ds.			XX	213 ACCACCAACCGCCACCTTTTCCAGAGCCCAACACCCCGGAGCCAGAGGAGATCCT 272
OS	Homo sapiens.			XX	277 ACCACCAACCGCCACCTTTTCCAGAGCCCAACACCCCGGAGCCAGAGGAGATCCT 336
				XX	273 GGGATCAGATGATGAGGAGCAAGAGACCTTGGGACTTACTGCAAGGTGGATATCATCC 332
				XX	337 GGGATCAGATGATGAGGAGCAAGAGACCTTGGGACTTACTGCAAGGTGGATATCATCC 396
				XX	333 AGTGAATAATGGAGACCTTTCAATGGCGGTATCATGTTATGAAGAGCTTGGATGGG 392
				XX	397 AGTGAATAATGGAGACCTTTCAATGGCGGTATCATGTTATGAAGAGCTTGGATGGG 456
				XX	393 GCATCTCTCTACTGCTGTGCTGGGATATGAGGGGAAAGATTTGTTGCAATGAA 452
				XX	457 GCATCTCTCTACTGCTGTGCTGGGATATGAGGGGAAAGATTTGTTGCAATGAA 516
				XX	453 AGTTGTAAAAAGTGGCCAGCATTATACGAGACACCTTGGATGAAATAAATTCCTCA 512
				XX	517 AGTTGTAAAAAGTGGCCAGCATTATACGAGACACCTTGGATGAAATAAATTCCTCA 576
				XX	513 ATGTGTTCCAGAAAGTGTATCCAGTGAACCAACAGACATGTTGTTGCTCAGCTCATTTGA 572

Db	577	ATGTGTTGAGAAAGTGATCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATTTGA	636
Qy	573	CGACTTCAAGATTTCAAGCATGATCGGATACATGCTGCTGATGGTCTTTCGAAGTACTTGG	632
Db	637	CGACTTCAAGATTTCAAGCATGATCGGATACATGCTGCTGATGGTCTTTCGAAGTACTTGG	696
Qy	633	CCACCATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCTCCCAAGTACGTTGCT	692
Db	697	CCACCATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCTCCCAAGTACGTTGCT	756
Qy	693	GAAGAGTATCATTTGCAAGGTCCTTCAAGGTTTGAATTAATTACACAGTAAGTGCAGAT	752
Db	757	GAAGAGTATCATTTGCAAGGTCCTTCAAGGTTTGAATTAATTACACAGTAAGTGCAGAT	816
Qy	753	CATTTCATCTGACATAAAGCCGAAATATCTTGATGCTGTGGATGATGCATATGTGAG	812
Db	817	CATTTCATCTGACATAAAGCCGAAATATCTTGATGCTGTGGATGATGCATATGTGAG	876
Qy	813	AAGAATGGCAGCTGAGGCCACCTGAGTGGCAGAAAGCAGGTGCTCTCTCTTCAAGGTC	872
Db	877	AAGAATGGCAGCTGAG--CCTGAGTGGCAGAAAGCAGGTGCTCTCTCTTCAAGGTC	933
Qy	873	TGAGTGAAGTACGGTCCACAGCAGAAACCTATPAGGAAAAATATCTAAAAACAAAAAGAA	932
Db	934	TGAGTGAAGTACGGTCCACAGCAGAAACCTATPAGGAAAAATATCTAAAAACAAAAAGAA	993
Qy	933	AAAACTGAAAAAGAAACAGAGGCGAGCTGAGTTATTTGGAGAGCGCTCGCAGAGAT	992
Db	994	AAAACTGAAAAAGAAACAGAGGCGAGCTGAGTTATTTGGAGAGCGCTCGCAGAGAT	1053
Qy	993	AGAAAGATTTGGAGCGAGAGCTGAAAGGAAATATATAGAGAAAAACATCACCTCAGCTGC	1052
Db	1054	AGAAAGATTTGGAGCGAGAGCTGAAAGGAAATATATAGAGAAAAACATCACCTCAGCTGC	1113
Qy	1053	ACCTTCCAATGACAGGATGGCGAATACCTGCCAGAGGTGAAATCTAAAAACAAACAGGAT	1112
Db	1114	ACCTTCCAATGACAGGATGGCGAATACCTGCCAGAGGTGAAATCTAAAAACAAACAGGAT	1173
Qy	1113	AGAGAGGCGGTGAGGCGAGAGCTGCAAAAGCAATGTGAGAGCTGAGGACAGAGAA	1172
Db	1174	AGAGAGGCGGTGAGGCGAGAGCTGCAAAAGCAATGTGAGAGCTGAGGACAGAGAA	1233
Qy	1173	GAAGAAGATGCTGAGAAAGAAAAATTCGAAAGATGAAGATGATGATAGATCAGAACT	1232
Db	1234	GAAGAAGATGCTGAGAAAGAAAAATTCGAAAGATGAAGATGATGATAGATCAGAACT	1293
Qy	1233	TGCGAATCATAGACCTTACGTGGATAGAAATCACCTAAAAACCAATGGCCATATTGAGAAATGG	1292
Db	1294	TGCGAATCATAGACCTTACGTGGATAGAAATCACCTAAAAACCAATGGCCATATTGAGAAATGG	1353
Qy	1293	CCCATTTCTCCTGGAGCAGAACTGGACGATGAAGATGATGAAGAAAGCTGGCCAAA	1352
Db	1354	CCCATTTCTCCTGGAGCAGAACTGGACGATGAAGATGATGAAGAAAGCTGGCCAAA	1413
Qy	1353	TCTGAGGAATATATCTTGTAGTGGCCAAATGACAGAAAGTATACACATATAGCAGCTC	1412
Db	1414	TCTGAGGAATATATCTTGTAGTGGCCAAATGACAGAAAGTATACACATATAGCAGCTC	1473
Qy	1413	CTATGAACCAATTCATGTGAAATTTGCCAAATGGACGACATAAAATTTCCCGAGTTCACAGTT	1472
Db	1474	CTATGAACCAATTCATGTGAAATTTGCCAAATGGACGACATAAAATTTCCCGAGTTCACAGTT	1533
Qy	1473	CCAGAGTTTCCACCTCGTTGTTCTCTGGATCTCTGATGCTGAGAACTGGCGCTCTGT	1532
Db	1534	CCAGAGTTTCCACCTCGTTGTTCTCTGGATCTCTGATGCTGAGAACTGGCGCTCTGT	1593
Qy	1533	GCTTTCTGAGGATCACCACTTACTGAGCAAGGAGAGCAGTCCATCCCATGACAGAG	1592
Db	1594	GCTTTCTGAGGATCACCACTTACTGAGCAAGGAGAGCAGTCCATCCCATGACAGAG	1653
Qy	1593	CAGAACGGTTTCAAGCTCTCAGTCTGGGATTTGCCAAAGCAAAACCCCGGAGCTGA	1652
Db	1654	CAGAACGGTTTCAAGCTCTCAGTCTGGGATTTGCCAAAGCAAAACCCCGGAGCTGA	1713
Qy	1653	CTTGTGTGTAATCCCTCGATCCGCGAATCGAGATAAAATTAGAGTAAAAATTTCTCTGA	1712
Db	1714	CTTGTGTGTAATCCCTCGATCCGCGAATCGAGATAAAATTAGAGTAAAAATTTCTCTGA	1773
Qy	1713	CCTGGGAAATGCTGTGGTGCATAAAACATCTTACCGAAGACATCCAGACGGCTCAGTA	1772
Db	1774	CCTGGGAAATGCTGTGGTGCATAAAACATCTTACCGAAGACATCCAGACGGCTCAGTA	1833
Qy	1773	CCGCTCCATPAGAGTTTAAATAGGAGCGGGTACAGACCCCTCGGGAATCTTGGAGCAC	1832
Db	1834	CCGCTCCATPAGAGTTTAAATAGGAGCGGGTACAGACCCCTCGGGAATCTTGGAGCAC	1893
Qy	1833	GGCGTATGTCATTTGAGCTGGCAACGGAGATATTTGTTGTTGAACCAATTTCTGGGA	1892
Db	1894	GGCGTATGTCATTTGAGCTGGCAACGGAGATATTTGTTGTTGAACCAATTTCTGGGA	1953
Qy	1893	AGACTATTTCAGAGACGAAGACCAATAGCCCAATCATAGAGCTGCTAGGAGATTTCC	1952
Db	1954	AGACTATTTCAGAGACGAAGACCAATAGCCCAATCATAGAGCTGCTAGGAGATTTCC	2013
Qy	1953	AAAGCACCTTGTCTATCTCGGAAATATTTCTCGGAAATTTCTTCAATCGCAGAGGAACT	2012
Db	2014	AAAGCACCTTGTCTATCTCGGAAATATTTCTCGGAAATTTCTTCAATCGCAGAGGAACT	2073
Qy	2013	GGGACACATCACAAGCTGAAGCCCTGGAGCCCTTTGATGCTACTTGTGGAAGATGCG	2072
Db	2074	GGGACACATCACAAGCTGAAGCCCTGGAGCCCTTTGATGCTACTTGTGGAAGATGCG	2133
Qy	2073	CTGGCCCATGAAGATGCTGCACAGTTTACAGATTTCTCTGATCCCGATGTTAGAAATGGT	2132
Db	2134	CTGGCCCATGAAGATGCTGCACAGTTTACAGATTTCTCTGATCCCGATGTTAGAAATGGT	2193
Qy	2133	TCCAGAAAAACGAGCTCAGCTGGCGAATTCCTCGGCATCTCTGGTGAATTTCTTAGCA	2192
Db	2194	TCCAGAAAAACGAGCTCAGCTGGCGAATG---TCGGCATCTCTGGTGAATTTCTTAGCA	2250
Qy	2193	AACTTCTACCAATTTGCAATTTGAGCTAGCAAAATGTTCCAGTACATTTGGACCTAAACGG	2252
Db	2251	AACTTCTACCAATTTGCAATTTGAGCTAGCAAAATGTTCCAGTACATTTGGACCTAAACGG	2310
Qy	2253	TCAGCTCTCATTTCTTAAACAGGATTAACAGTGAAGCTTTCATCTCAGACCTTTATTTT	2312
Db	2311	TCAGCTCTCATTTCTTAAACAGGATTAACAGTGAAGCTTTCATCTCAGACCTTTATTTT	2370
Qy	2313	GCTTTGAGTACTGTTGTTGATGCTTTTGTGACATTTGTCACCTGTGATCTCTGGGAGGGT	2372
Db	2371	GCTTTGAGTACTGTTGTTGATGCTTTTGTGACATTTTGTGACCTGTGATCTCTGGGAGGGT	2430
Qy	2373	AGTCTTTTGTCTTCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT	2432
Db	2431	AGTCTTTTGTCTTCAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT	2490
Qy	2433	CTCTAAGCATTTCTTGTGTTGTGACATTTCAAAATGTCATTTTGTGAAATGAAAAAT	2492
Db	2491	CTCTAAGCATTTCTTGTGTTGTGACATTTCAAAATGTCATTTTGTGAAATGAAAAAT	2550
Qy	2493	ACTTTCCCTTTGCTTTTGGCAGGTTTGTAACTATTATTAAGAAAAATTTTGTAGCTGA	2552
Db	2551	ACTTTCCCTTTGCTTTTGGCAGGTTTGTAACTATTATTAAGAAAAATTTTGTAGCTGA	2610
Qy	2553	GTACTATATAATTAACAATTTTAAAGAAATTTTCAAGTGTGGGAAACCAAGAAAAATAGCAAG	2612
Db	2611	GTACTATATAATTAACAATTTTAAAGAAATTTTCAAGTGTGGGAAACCAAGAAAAATAGCAAG	2667
Qy	2613	GAATGTACAAATTTTATCTTCTGGCAAGGAGGACATCTTCTGTTATATAGTGTATGTA	2672
Db	2668	GAATGTACAAATTTTATCTTCTGGCAAGGAGGACATCTTCTGTTATATAGTGTATGTA	2727
Qy	2673	ATGCCACCTGTAAATGTTTACTTTGATTTAAATATGCGGAGGGGAGCTCAAAATTTAGAAA	2732
Db	2728	ATGCCACCTGTAAATGTTTACTTTTCCATTAATATGGA--GGGGAGCTCAAAATTTAGAAA	2786

QY	2733	AGCTAAAAA 2741	QY	213	ACCACCAACCCGACCTTTTCCAGACCCCAACCCCGGAGCCAGAGAGAGATCCT	272
Db	2787	AGCTACCAA 2795	Db	277	ACCAACCAACCCGACCTTTTCCAGACCCCAACCCCGGAGCCAGAGAGAGATCCT	336
QY	2733	AGCTAAAAA 2741	QY	273	GGGATCAGATGATGAGGAGCAAGAGACCTTGGGACTACTGCAAGGTTGGATATCATCC	332
Db	2787	AGCTACCAA 2795	Db	337	GGGATCAGATGATGAGGAGCAAGAGACCTTGGGACTACTGCAAGGTTGGATATCATCC	396
QY	2733	AGCTAAAAA 2741	QY	333	AGTGAAAAATTTGGAGACCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG	392
Db	2787	AGCTACCAA 2795	Db	397	AGTGAAAAATTTGGAGACCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG	456
QY	2733	AGCTAAAAA 2741	QY	393	GCATTTCTCTACTGTCTGGCTGTGCTGGATATGAGGGGAAAGATTTTGGCAATGAA	452
Db	2787	AGCTACCAA 2795	Db	457	GCATTTCTCTACTGTCTGGCTGTGCTGGATATGAGGGGAAAGATTTTGGCAATGAA	516
QY	2733	AGCTAAAAA 2741	QY	453	AGTTGTAAGGAGTCCAGCATTTATACGAGACAGCCTTGTGATGAAATAAATTTGCTCAA	512
Db	2787	AGCTACCAA 2795	Db	517	AGTTGTAAGGAGTCCAGCATTTATACGAGACAGCCTTGTGATGAAATAAATTTGCTCAA	576
QY	2733	AGCTAAAAA 2741	QY	513	ATGTGTTTCGAGAAAGTGTATCCAGTGACCCAAACAAAGACATGGTGTCCAGCTCATTTGA	572
Db	2787	AGCTACCAA 2795	Db	577	ATGTGTTTCGAGAAAGTGTATCCAGTGACCCAAACAAAGACATGGTGTCCAGCTCATTTGA	636
QY	2733	AGCTAAAAA 2741	QY	573	CGACTTCAAGATTTTCAGGCATGAAATGGGATACATGTCTGATGGTCTTTCGAAGTACTTGG	632
Db	2787	AGCTACCAA 2795	Db	637	CGACTTCAAGATTTTCAGGCATGAAATGGGATACATGTCTGATGGTCTTTCGAAGTACTTGG	696
QY	2733	AGCTAAAAA 2741	QY	633	CCACCATCTCTCAAGTGGATCATCAATCAACTATCAAGGCCCTCCAGTACCTTGTGT	692
Db	2787	AGCTACCAA 2795	Db	697	CCACCATCTCTCAAGTGGATCATCAATCAACTATCAAGGCCCTCCAGTACCTTGTGT	756
QY	2733	AGCTAAAAA 2741	QY	693	GAAGAGTATCATTCGACAGGTCCTTCAAGGTTTATGATTTACATGATAGTGCAGAT	752
Db	2787	AGCTACCAA 2795	Db	757	GAAGAGTATCATTCGACAGGTCCTTCAAGGTTTATGATTTACATGATAGTGCAGAT	816
QY	2733	AGCTAAAAA 2741	QY	753	CATTCTACTGACATTAAGCCGGAATATCTTCATGCTGTGTGATGATGATGATGATG	812
Db	2787	AGCTACCAA 2795	Db	817	CATTCTACTGACATTAAGCCGGAATATCTTCATGCTGTGTGATGATGATGATGATG	876
QY	2733	AGCTAAAAA 2741	QY	813	AAGAAATGCGAGTGGGCTGAGTGGCAGAAAGCAGGTCCTCTCTCTCTCAGGTC	872
Db	2787	AGCTACCAA 2795	Db	877	AAGAAATGCGAGTGGGCTGAGTGGCAGAAAGCAGGTCCTCTCTCTCTCAGGTC	933
QY	2733	AGCTAAAAA 2741	QY	873	TGCAGTGTAGTACGGCTCCACAGAGAAACCTTATAGGAAATAATCTAATAAACAAGAA	932
Db	2787	AGCTACCAA 2795	Db	934	TGCAGTGTAGTACGGCTCCACAGAGAAACCTTATAGGAAATAATCTAATAAACAAGAA	993
QY	2733	AGCTAAAAA 2741	QY	933	AAAATCTGAAAGAAACAGAGAGCGGCTGAGTTATTGGAGAGCGCTGCGAGGAT	992
Db	2787	AGCTACCAA 2795	Db	994	AAAATCTGAAAGAAACAGAGAGCGGCTGAGTTATTGGAGAGCGCTGCGAGGAT	1053
QY	2733	AGCTAAAAA 2741	QY	993	AGAAGAAATTTGAGGAGAGGCTGAAAGGAAATAATAGAGAAACATCATCTCAGTGC	1052
Db	2787	AGCTACCAA 2795	Db	1054	AGAAGAAATTTGAGGAGAGGCTGAAAGGAAATAATAGAGAAACATCATCTCAGTGC	1113
QY	2733	AGCTAAAAA 2741	QY	1053	ACCTTCCAAATGACAGGATGGGATATCTGCCAGAGTGAACCTTAAACCAACAGGAT	1112
Db	2787	AGCTACCAA 2795	Db	1114	ACCTTCCAAATGACAGGATGGGATATCTGCCAGAGTGAACCTTAAACCAACAGGAT	1173
QY	2733	AGCTAAAAA 2741	QY	1113	AGAGAGGCGGCTGAGGAGAGCTGCAAGGACAAATGCTGAAGCTGAGGACCCAGGAAGA	1172
Db	2787	AGCTACCAA 2795	Db	1174	AGAGAGGCGGCTGAGGAGAGCTGCAAGGACAAATGCTGAAGCTGAGGACCCAGGAAGA	1233
QY	2733	AGCTAAAAA 2741	QY	1173	GAAGAAGATGCTGAGAAAGAAACATTTGAAAGATGAAGATGATGATGATGATGATG	1232
Db	2787	AGCTACCAA 2795	Db	1234	GAAGAAGATGCTGAGAAAGAAACATTTGAAAGATGAAGATGATGATGATGATGATG	1293
QY	2733	AGCTAAAAA 2741	QY	1233	TCCGAACATAGACCTTACGTCGATGATGATGATGATGATGATGATGATGATGATG	1292
Db	2787	AGCTACCAA 2795	Db	1294	TCCGAACATAGACCTTACGTCGATGATGATGATGATGATGATGATGATGATGATG	1353
QY	2733	AGCTAAAAA 2741	QY	1293	CCCATTCTCACTGGAGCAGCACTGAGCGATGATGATGATGATGATGATGATGATG	1352

RESULT 9
 ADO19346
 ID ADO19346 standard; cDNA; 3745 BP.
 AC ADO19346;
 XX 12-AUG-2004 (first entry)
 DE Human PRO polynucleotide #139.
 KW Human; PRO; gene; ss; immune related disorder;
 KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
 KW juvenile chronic arthritis; systemic sclerosis; Sjogren's syndrome;
 KW vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
 KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
 KW renal disease; demyelinating disease; central nervous system;
 KW peripheral nervous system; demyelinating polyneuropathy;
 KW Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.
 OS Homo sapiens.
 XX WO2004043361-A2.
 XX 27-MAY-2004.
 XX 06-NOV-2003; 2003WO-US035268.
 XX 08-NOV-2002; 2002US-0425235P.
 XX (GETH) GENENTECH INC.
 XX Fong S, Dennis K, Clark H, Chiu H, Schoenfeld J, Williams PM;
 XX Wood WI, Wu TD;
 XX WPI; 2004-420067/39.
 XX P-PSDB; ADO19347.
 XX Novel PRO polypeptide e.g., PRO69614, PRO71106, or PRO86388 useful for
 XX treating an immune related disorder such as systemic lupus erythematosus,
 XX rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis or
 XX spondyloarthritis.
 XX Claim 1; SEQ ID NO 288; 1731pp; English.
 XX The invention relates to human PRO polypeptides and the polynucleotides
 XX encoding them. The polypeptides and polynucleotides are useful for
 XX treating and diagnosing immune related disorders in mammals. The immune
 XX related disorders include systemic lupus erythematosus, rheumatoid
 XX arthritis, osteoarthritis, juvenile chronic arthritis, systemic
 XX sclerosis, Sjogren's syndrome, vasculitis, sarcoidosis, autoimmune
 XX haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes
 XX mellitus, immune-mediated renal disease, demyelinating diseases of the
 XX central or peripheral nervous system, demyelinating polyneuropathy,
 XX Guillain-Barre syndrome and chronic inflammatory demyelinating
 XX polyneuropathy. This sequence represents a human PRO polynucleotide of
 XX the invention.
 SQ Sequence 3745 BP; 1163 A; 719 C; 829 G; 1034 T; 0 U; 0 Other;
 Query Match 76.8%; Score 2497; DB 12; Length 3745;
 Best Local Similarity 98.8%; Pred. No. 0;
 Matches 2559; Conservative 0; Mismatches 20; Indels 10; Gaps 4;
 QY 153 TCCGAAAAAGCCGAGGCTCAACAGAAAGCTCTTAGTTCTCTCTCCACCGCCACC 212
 Db 217 TTCAGAAAGCCGAGGCTCAACAGAAAGCTCTTAGTTCTCTCTCCACCGCCACC 276

1354 DB CCCATCTCAGTGGAGCAACTGACCGATGAAGATGATGAAGAGACTGCCCAA 1413
1353 QY TCTGAGGAATATAATCTTTGATGAGCCAAATGCGAAAGTGAATACACATATAGCAGTTC 1412
1414 DB TCTGAGGAATATAATCTTTGATGAGCCAAATGCGAAAGTGAATACACATATAGCAGTTC 1473
1413 QY CTATGAACAATTCATATGGTGAATTCGCAATGCGACATATAAATTCGCCAGTTCACAGTT 1472
1474 DB CTATGAACAATTCATATGGTGAATTCGCAATGCGACATATAAATTCGCCAGTTCACAGTT 1533
1473 QY CCCAGAGTTTCCACCTCGTGTCTCTGGATCCTTAGAACCTGTGGCCCTGGCGGTCTGT 1532
1534 DB CCCAGAGTTTCCACCTCGTGTCTCTGGATCCTTAGAACCTGTGGCCCTGGCGGTCTGT 1593
1533 QY GCTTTCTGAGGATACCACTTACTGAGCAAGAGGAGAGCGTCCATCCCATGACAGAAG 1592
1594 DB GCTTTCTGAGGATACCACTTACTGAGCAAGAGGAGAGCGTCCATCCCATGACAGAAG 1653
1593 QY CAGAACGGTTTCAGCCTCCAGTACTGGGATTTGCCAAGACAAACCCGGGCGACTGA 1652
1654 DB CAGAACGGTTTCAGCCTCCAGTACTGGGATTTGCCAAGACAAACCCGGGCGACTGA 1713
1653 QY CTGTGTGGTGAATCCCTCGATCCGCGAATGCGAGATAAATTTAGAGTAAATTTGCTGA 1712
1714 DB CTGTGTGGTGAATCCCTCGATCCGCGAATGCGAGATAAATTTAGAGTAAATTTGCTGA 1773
1713 QY CTGTGGAAATGCTGTGTGGTGCATAAACACTTCACGGAGACATCCAGACCGCTCAGTA 1772
1774 DB CTGTGGAAATGCTGTGTGGTGCATAAACACTTCACGGAGACATCCAGACCGCTCAGTA 1833
1773 QY CCGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTGGGACATCTGGAGCAC 1832
1834 DB CCGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTGGGACATCTGGAGCAC 1893
1833 QY CGCGTGTATGGCATTTGAGCTGCGAACGGGAGATTTATTTGTTGAACCACTTCTGGGGA 1892
1894 DB GCGGTGTATGGCATTTGAGCTGCGAACGGGAGATTTATTTGTTGAACCACTTCTGGGGA 1953
1893 QY AGACTATTCCAGAGAGCAAGACCAATAGCACCACATCATAGAGCTGTAGGAGTATTC 1952
1954 DB AGACTATTCCAGAGAGCAAGACCAATAGCACCACATCATAGAGCTGTAGGAGTATTC 2013
1953 QY AAGGCATTTGCTCTATCTGGAATAATTTCTCGGGAATTTCTCAATCGCAGAGGAATC 2012
2014 DB AAGGCATTTGCTCTATCTGGAATAATTTCTCGGGAATTTCTCAATCGCAGAGGAATC 2073
2013 QY GCGACACATCACAGCTCAAGCCCTGGAGCCTCTTTGATGTACTTTGTGAAAGTATCG 2072
2074 DB GCGACACATCACAGCTCAAGCCCTGGAGCCTCTTTGATGTACTTTGTGAAAGTATCG 2133
2073 QY CTGGCCCATGAAGATGCTGCGACAGTTTACAGATTTCTCTGATCCCGATTTAGAAATGTT 2132
2134 DB CTGGCCCATGAAGATGCTGCGACAGTTTACAGATTTCTCTGATCCCGATTTAGAAATGTT 2193
2133 QY TCCAGAAAACGAGCCTCAGCTGGGGAATGCGCTTCGGGATCCTGTGAAATCTTTAGCA 2192
2194 DB TCCAGAAAACGAGCCTCAGCTGGGGAATG---TCGGCATCCTTGGTTGAATCTTTAGCA 2250
2193 QY AATTTACCAATATTGCAATCTGAGCTAGCAATGTTCCAGTACATTTGAGCCTAAACGG 2252
2251 DB AATTTACCAATATTGCAATCTGAGCTAGCAATGTTCCAGTACATTTGAGCCTAAACGG 2310
2253 QY TGACTCTCATTTCTTAAACAGGATTACAAGTGAAGTGGCTTCTCATCTCAGACCTTTATTTT 2312
2311 DB TGACTCTCATTTCTTAAACAGGATTACAAGTGAAGTGGCTTCTCATCTCAGACCTTTATTTT 2370
2313 QY GCTTTGAGTACTGTTGTTTGAATTTGCTTTTGTGCACTGTGATCTCGGGAGGGT 2372
2371 DB GCTTTGAGTACTGTTGTTTGAATTTGCTTTTGTGCACTGTGATCTCGGGAGGGT 2430
2373 QY AGCTTTTGTCTTCAGCTAAGTATTTACTGACCATTTTCTTCTGGAACAATATCATGT 2432

2431 DB AGTCTTTTGTCTTCAGCTAAGTAGTTTACTGACCATTTTCTTCTGGAACAATAACATGT 2490
2433 QY CTCTAAGCAATGTTCTTCTGTGTGTGACATTTCAAAATGTCATTTTGTGAATGAAAAAT 2492
2491 DB CTCTAAGCAATGTTCTTCTGTGTGTGACATTTCAAAATGTCATTTTGTGAATGAAAAAT 2550
2493 QY ACTTTCCCTTTGCTGTTTGGCAGGTTTGTAACTATTTATGAAGAAATATTTTACCTGA 2552
2551 DB ACTTTCCCTTTGCTGTTTGGCAGGTTTGTAACTATTTATGAAGAAATATTTTACCTGA 2610
2553 QY GTACTATATAATTTCAATCTTTAAGAAATTTCAAGTTTGGGAACCAAGAAAAATAGCAAG 2612
2611 DB GTACTATATAATTTCAATCTTTAAGAAATTTCAAGTTTGGGAACCAAGAAAAATAGCAAG 2667
2613 QY GAAATGTACAATTTTATCTCTGGCAAGGGAACATCATTTCTCTGTATATAGTGTATGTAA 2672
2668 DB GAAATGTACAATTTTATCTCTGGCAAGGGAACATCATTTCTCTGTATATAGTGTATGTAA 2727
2673 QY ATGCACCTCTGTAATGTTTACTTTGGATTAAATATGAGGGGGGACTCAAAATTTTCAGAAA 2732
2728 DB ATGCACCTCTGTAATGTTTACTTTCCATTAAATATGGA--GGGGGACTCAAAATTTTCAGAAA 2786
2733 QY AGCTAAAAA 2741
2787 DB AGCTACCAA 2795
RESULT 10
AAL54217
ID AAL54217 standard; DNA; 2094 BP.
XX AC AAL54217;
XX DT 27-MAR-2003 (first entry)
XX SR protein-specific kinase-1 DNA, SEQ ID No 9.
XX DE Cytostatic; p53 pathway-modulating agent; SR protein; cancer; apoptosis;
XX KW lung cancer; breast cancer; serine/arginine protein-specific kinase;
XX KW colon cancer; ovarian cancer; SRPK; cell proliferation; human; ds.
XX OS Homo sapiens.
XX PN WO200299427-A1.
XX PD 12-DEC-2002.
XX PX 03-JUN-2002; 2002WO-US017525.
XX PR 05-JUN-2001; 2001US-0296076P.
XX PR 10-OCT-2001; 2001US-0328605P.
XX PR 15-FEB-2002; 2002US-0357253P.
XX PA (EXEL-) EXELIXIS INC.
XX PI Friedman L, Florman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
XX WP1; 2003-156865/15.
XX PT Identifying candidate p53 pathway-modulating agents useful as therapeutic
XX PT targets for disorders related with defective p53 function, by screening
XX PT for agents modulating serine/arginine protein-specific kinase activity.
XX PS Disclosure; Page 114-115; 137pp; English.
XX CC The invention relates to a novel method for identifying candidate p53
XX CC pathway-modulating agents. The novel method comprises screening for
XX CC agents that modulate the activity of a serine/arginine protein-specific
XX CC kinase. The invention provides methods for utilizing p53 modifier genes
XX CC and polypeptides to identify candidate therapeutic agents that can be
XX CC used in the treatment of disorders associated with defective p53
XX CC function. The methods are also useful for modulating a p53 pathway in a
XX CC mammalian cell, or for diagnosing or treating a disease associated with

defective p53 function, e.g. cancers such as breast cancer, colon cancer, lung cancer or ovarian cancer. The serine/arginine protein-specific kinase (SRPK) polypeptides and nucleic acids are useful for identifying and testing agents that modulate SRPK function. The animal models are useful for in vivo assays to test the activity of a candidate p53-modulating agent, or to assess the role of SRPK in a p53 pathway process such as apoptosis or cell proliferation. This polynucleotide sequence represents the DNA of a serine/arginine-rich domain protein-specific kinase-1 of the invention

Sequence 2094 BP; 652 A; 458 C; 526 G; 458 T; 0 U; 0 Other;

Query Match 62.7%; Score 2039.6; DB 8; Length 2094;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 2042;	Conservative	0;	Mismatches	4;	Indels	0;	Gaps	0;
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Qy	153	TCCGAAAAAGCCCGAGCCTCAACAGAAAGCTCCTTTAGTTCTCTCTCTCTCACCGCCACC	213
Db	49	TTCAAGAAAGCCCGAGCCTCAACAGAAAGCTCCTTTAGTTCTCTCTCTCTCACCGCCACC	108
Qy	213	ACCACCACCCGCGACCTTTGGCAGACCCACACCCCGGAGCCAGAGGAGAGATCCT	272
Db	109	ACCACCACCCGCGACCTTTGGCAGACCCACACCCCGGAGCCAGAGGAGAGATCCT	168
Qy	273	GGGATCAGATGATCAGGAGCAGAGGACCCCTGCGGACTATCGCAAAGGTGGATATCATCC	332
Db	169	GGGATCAGATGATCAGGAGCAGAGGACCCCTGCGGACTATCGCAAAGGTGGATATCATCC	228
Qy	333	AGTGAAAAATGGAGACCTCTTCAATGCCGGTATCATGTTATTAGAAAGCTTGGATGGG	392
Db	229	AGTGAAAAATGGAGACCTCTTCAATGCCGGTATCATGTTATTAGAAAGCTTGGATGGG	288
Qy	393	GCATCTCTACTGTCTGGCTGTCTGGGATATGACGGGGAAAAAGATTGTTGCAATGAA	452
Db	289	GCATCTCTACTGTCTGGCTGTCTGGGATATGACGGGGAAAAAGATTGTTGCAATGAA	348
Qy	453	AGTTGTAAAAAGTCCAGCATTTATACGGAGACGCTTGGATGAAATATAAATTTCCTCAA	512
Db	349	AGTTGTAAAAAGTCCAGCATTTATACGGAGACGCTTGGATGAAATATAAATTTCCTCAA	408
Qy	513	ATGTGTTTCGAAAAAGTATCCAGTGACCCAAAAAAGACATGTTGGTCCAGCTCATTTGA	572
Db	409	ATGTGTTTCGAAAAAGTATCCAGTGACCCAAAAAAGACATGTTGGTCCAGCTCATTTGA	468
Qy	573	CGACTTCAAGATTTTCAAGCATGAATGGGATATGTCGCATGTCCTTTCGAAGTACTTGG	632
Db	469	CGACTTCAAGATTTTCAAGCATGAATGGGATATGTCGCATGTCCTTTCGAAGTACTTGG	528
Qy	633	CCACCATCTCTCAAGTGGATCATCAATCCAACTATCAAGGCCTCCAGTACGTTGTTGT	692
Db	529	CCACCATCTCTCAAGTGGATCATCAATCCAACTATCAAGGCCTCCAGTACGTTGTTGT	588
Qy	693	GAAGATATCATTTTCGACAGGTCTTTCAAGGGTTAGATTACTTTACACAGTAAGTCAAGAT	752
Db	589	GAAGATATCATTTTCGACAGGTCTTTCAAGGGTTAGATTACTTTACACAGTAAGTCAAGAT	648
Qy	753	CATTTCATCTGACATAAAGCCGAAAAATATCTTGTATGTGTGTGGATGATGATATGTGAG	812
Db	649	CATTTCATCTGACATAAAGCCGAAAAATATCTTGTATGTGTGTGGATGATGATATGTGAG	708
Qy	813	AAGAAATGCGAGTGAAGCCACTGAGTGGCAGAAAGCAGTGTCTCTCTCTTCAGGGTTC	872
Db	709	AAGAAATGCGAGTGAAGCCACTGAGTGGCAGAAAGCAGTGTCTCTCTCTTCAGGGTTC	768
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Db 2089 AATTCT 2094
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ID AAL54216 standard; DNA; 1956 BP.
XX AAL54216;
AC AAL54216;
DT 27-MAR-2003 (first entry)
XX SR protein-specific kinase-1 DNA, SEQ ID No 8.
DE
XX Cytostatic; p53 pathway-modulating agent; SR protein; cancer; apoptosis;
KW lung cancer; breast cancer; serine/arginine protein-specific kinase;
KW colon cancer; ovarian cancer; SRPK; cell proliferation; human; ds.
XX Homo sapiens.
XX WO200299427-A1.
PN
XX 12-DEC-2002.
XX
XX 03-JUN-2002; 2002WO-US017525.
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XX 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 15-FEB-2002; 2002US-0357253P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Friedman L, Plozman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI WPI; 2003-156865/15.
XX
XX
XX Identifying candidate p53 pathway-modulating agents useful as therapeutic
PT targets for disorders related with defective p53 function, by screening
PT for agents modulating serine/arginine protein-specific kinase activity.
XX
XX Disclosure; Page 113-114; 137pp; English.
PS
XX The invention relates to a novel method for identifying candidate p53
CC pathway-modulating agents. The novel method comprises screening for
CC agents that modulate the activity of a serine/arginine protein-specific
CC kinase. The invention provides methods for utilizing p53 modifier genes
CC and polypeptides to identify candidate therapeutic agents that can be
CC used in the treatment of disorders associated with defective p53
CC function. The methods are also useful for modulating a p53 pathway in a
CC mammalian cell, or for diagnosing or treating a disease associated with
CC defective p53 function, e.g. cancers such as breast cancer, colon cancer,
CC lung cancer or ovarian cancer. The serine/arginine protein-specific
CC kinase (SRPK) polypeptides and nucleic acids are useful for identifying
CC and testing agents that modulate SRPK function. The animal models are
CC useful for in vivo assays to test the activity of a candidate p53-
CC modulating agent, or to assess the role of SRPK in a p53 pathway process
CC such as apoptosis or cell proliferation. This polynucleotide sequence
CC represents the DNA of a serine/arginine-rich domain protein-specific
CC kinase-1 of the invention
XX
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Query Match 53.9%; Score 1753.6; DB 8; Length 1956;
Best Local Similarity 93.1%; Pred. No. 0;
Matches 1904; Conservative 0; Mismatches 4; Indels 138; Gaps 1;

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QY 393 GCACCTTCTACTGCTGGTGTGGATATGAGGAGGAAAAGATTTTGGCAATGAA 452
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2394 CATCAGGAAGCAAAACCCGGGCGAGCTGACTTTGTGTGTAATCCCTCTGATCCGCGAA 2453
1683 TGCAGATAAATTTAGAGTAAATTTGCTGACCTGGGAAATGCTTTGTTGGTGCATAAACA 1742
2454 TGCAGATAAATTTAGAGTAAATTTGCTGACCTGGGAAATGCTTTGTTGGTGCATAAACA 2513
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RESULT 13

ADN98453

ID ADN98453 standard; cDNA; 1005 BP.

XX

AC ADN98453;

XX

XX 29-JUL-2004 (first entry)

XX

XX Novel human cDNA sequence #53.

DE

KW ds; gene; anti-inflammatory; dermatological; neuroprotective;

KW immunomodulator; antibacterial; virucide; antipsoriatic; cytostatic;

KW gene therapy; vaccine; inflammatory; CNS; immune disorder; cancer;

KW psoriasis; diabetes; early aging; hormonal imbalance;

KW ischemic heart disease; ulcerative colitis.

XX

OS Homo sapiens.

XX

XX WO2004038003-A2.

PN

XX 06-MAY-2004.

XX

XX 24-OCT-2003; 2003WO-US033947.

XX

XX 25-OCT-2002; 2002US-0421061P.

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OM nucleic - nucleic search, using sw model

Run on: January 23, 2005, 05:50:23 ; Search time 13465 Seconds
(without alignments)
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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ALIGNMENTS

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 AR265348 ACCESSION
 AR265348.1 GI:29693850
 VERSION
 AR265348.1
 KEYWORDS
 Unknown.
 SOURCE
 Unknown.
 ORGANISM
 Unclassified.
 REFERENCE 1. (bases 1 to 3253)
 AUTHORS Abu-Threideh, J., Gong, F., Ketchum, K.A., Di Francesco, V. and
 Beasley, E.M.
 TITLE Isolated human kinase proteins, nucleic acid molecules encoding
 human kinase proteins, and uses thereof
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DEFINITION Sequence 1 from Patent WO02057458.
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VERSION AX666205.1 GI:29291001
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1
AUTHORS Yan,C., Abu-Threideh,J., Shao,W., Merkllov,G., di Francesco,V. and Beasley,E.M.

TITLE Isolated human kinase proteins, nucleic acid molecules encoding human kinase proteins, and uses thereof
JOURNAL Patent: WO 02057458-A 1 25-JUL-2002;
PE Corporation (NY) (US)
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Best Local Similarity 100.0%; Pred. No. 0;
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AUTHORS
TITLE
JOURNAL

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Bandman, O., Hillman, J. L., Lal, P., Akerblom, I. E., Shah, P.,
Corley, N. C. and Guegler, K. J.
Protein kinase molecules
Patent: US 5962232-A 8 05-OCT-1999;

Unclassified.

ORIGIN

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RESULT 4
BD107902 2791 bp DNA linear PAT 18-SEP-2002
LOCUS Protein kinase molecules.
DEFINITION BD107902
ACCESSION BD107902
VERSION BD107902.1 GI:23202720
KEYWORDS JP 2002501749-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2791)
AUTHORS Bandman,O., Hillman,J.L., Lal,P., Akerblom,I.E., Shah,P.,
Corley,N.C. and Guegler,K.J.
TITLE Protein kinase molecules
JOURNAL Patent: JP 2002501749-A 2 22-JAN-2002;
COMMENT INCYTE PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002501749-A/2
PD 22-JAN-2002
PF 12-JAN-1999 JP 2000529440
PR 30-JAN-1998 US 09/016000
PI OLGA BANDMAN, JENNIFER L HILLMAN, PREETI LAL, INGRID E AKERBLOM,
PI PURVI SHAH.
PI NEIL C CORLEY, KARL J GUEGLER
PC C12N15/09,A61K38/45,A61K45/00,C07K16/40,C12N1/15,C12N1/19, PC
C12N1/21,
PC C12N5/10,C12N9/12,C12Q1/68,G01N33/68,C12N15/00,A61K37/52,C12N5/ PC
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FEATURES
source
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Best Local Similarity 97.0%; Pred. No. 0;
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QY 2351 CACTGTGATCTCTGGGGAAGGTAGTCTTTTGTCTTCAAGTAAAGTACTGACCAATTT 2410

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Db	423	GCACCTTCTCTACTGTCTGCTGCTGGGATATGCAAGGGGAAAAGATTTGTCATGAA	482
QY	453	AGTTGTAAAGGTGCCAGCATTTATACGGAGACAGCCTTTGGATGAAATAAAATTTGCTCAA	512
Db	483	AGTTGTAAAGGTGCCAGCATTTATACGGAGACAGCCTTTGGATGAAATAAAATTTGCTCAA	542
QY	513	ATGTGTTTCAGAAAGTGATCCAGTGACCCCAACAAAGACATGGTGGTCCAGCTANTGA	572
Db	543	ATGTGTTTCAGAAAGTGATCCAGTGACCCCAACAAAGACATGGTGGTCCAGCTANTGA	602
QY	573	CGACTTCAAGATTTTCAGGCATGAATGGGATACATGTCATCGATGCTTCCGAAGTACTGG	632
Db	603	CGACTTCAAGATTTTCAGGCATGAATGGGATACATGTCATCGATGCTTCCGAAGTACTGG	662
QY	633	CCACCATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCCAAGTACTGGT	692
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QY	753	CATTCTACTGCATAAAGCCGGAATAATCTTGTGTGTGGATGATGCATATGTGAG	812
Db	783	CATTCTACTGCATAAAGCCGGAATAATCTTGTGTGTGGATGATGCATATGTGAG	842
QY	813	AAGAAATGGCAGCTGAGGCCACCTGAGTGGCAGAAAGCAGGTGCTCTCTCTCCAGGGTC	872
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QY	873	TGCAGTGAGTACGGCTTCCACAGAGAAACCTTATAGGAAAAATATCTTAAAAACAAAAGAA	932
Db	903	TGCAGTGAGTACGGCTTCCACAGAGAAACCTTATAGGAAAAATATCTTAAAAACAAAAGAA	962
QY	933	AAAACTGAAAAAGAACAGAGGCGAGCTGAGTTATTGGAGAGCGGCTCCAGAGAT	992
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RESULT 7
AX666550
LOCUS
DEFINITION
SEQUENCE 3 from Patent WO02094796.
ACCESSION
AX666550
VERSION
AX666550.1 GI:29291032
KEYWORDS
SOURCE
ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
Pato, J., Keri, G., Oerfi, L., Waczek, F., Horvath, Z., Banhegyi, P., Szabadkai, I., Marosfalvi, J., Hegymegi-Barakonyi, B., sz Kelyhidi, Z., Greff, Z., Choldas, A., Bacher, G., Daub, H., Obert, S., Kurtenbach, A., and Habenberger, P.
TITLE
Benzo[g]quinoxaline derivatives as effective compounds against infectious diseases
JOURNAL
Patent: WO 02094796-A 3 28-NOV-2002;
Axxima Pharmaceuticals Aktiengesellschaft (DE)
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Location/Qualifiers
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Matches 2559; Conservative 0; Mismatches 20; Indels 10; Gaps 4;
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Db 217 TTCAGAAAGCCGAGCCTCAACAGAAAGCTCCTTTAGTTCTCTCTCCACCGCCACC 276
Qy 213 ACCACACACCCGACCTTTGCCAGACCCCAACCCCGAGCCAGAGAGAGATCCT 272
Db 277 ACCACACACCCGACCTTTGCCAGACCCCAACCCCGAGCCAGAGAGAGATCCT 336
Qy 273 GGGATCAGATGATGAGGACAGAGAGCCCTCGGACTACTGCAAGGTGGATATCATCC 332
Db 337 GGGATCAGATGATGAGGACAGAGAGCCCTCGGACTACTGCAAGGTGGATATCATCC 396
Qy 333 AGTGAATAATGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 392
Db 397 AGTGAATAATGGAGACCTCTTCAATGGCCGGTATCATGTTATTAGAAAGCTTGGATGGG 456
Qy 393 GCACCTTCTACTGTCTGTGCTGTGGATATGCAAGGGAAAAAGATTTTGTGCAATGAA 452
Db 457 GCACCTTCTACTGTCTGTGCTGTGGATATGCAAGGGAAAAAGATTTTGTGCAATGAA 516
Qy 453 AGTTGTAAAAAGTGGCCAGCATTTATCGGAGACAGCCTTTGGATGAATAAATTTGCTCAA 512
Db 517 AGTTGTAAAAAGTGGCCAGCATTTATACGGAGACAGCCTTTGGATGAATAAATTTGCTCAA 576
Qy 513 ATGTGTTCCAGAAAGTGTCCAGTGACCCAAACAAAGACATGTTGGTCCAGCTCAATGA 572
Db 577 ATGTGTTCCAGAAAGTGTCCAGTGACCCAAACAAAGACATGTTGGTCCAGCTCAATGA 636
Qy 573 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTGCATGGTCTTCGAACTCTTGG 632
Db 637 CGACTTCAAGATTTTCAGGCATGAATGGGATACATGCTGCATGGTCTTCGAACTCTTGG 696
Qy 633 CCACCATCTCTCAAGTGGATCATCAAATCCAACTATCAAGGCCTCCAGTACGTTGTGT 692
Db 697 CCACCATCTCTCAAGTGGATCATCAAATCCAACTATCAAGGCCTCCAGTACGTTGTGT 756
Qy 693 GAAGAGTATCATTCGACAGGTCCTTCAAGGGTTAGATTACTTACACAGTAAGTGAAGAT 752
Db 757 GAAGAGTATCATTCGACAGGTCCTTCAAGGGTTAGATTACTTACACAGTAAGTGAAGAT 816

693 QY GAAGAGTATCATTCGACAGTCTCTTCAAGSGTTAGATTACTTACACAGTAAGTGAAGAT 752
742 Db GAAGAGTATCATTCGACAGTCTCTTCAAGSGTTAGATTACTTACACAGTAAGTGAAGAT 801
753 QY CATTTACTGACATAAAGCCGGAATAATCTTTGATGTGTGGATGATGCATATGTGAG 812
802 Db CATTTACTGACATAAAGCCGGAATAATCTTTGATGTGTGGATGATGCATATGTGAG 861
813 QY AAGATGGAGCTGAGGCCACCTGAGTGGCAGAAAGCAGGTGCTCTCTCTTCAGGGTC 872
862 Db AAGATGGAGCTGAGGCCACCTGAGTGGCAGAAAGCAGGTGCTCTCTCTTCAGGGTC 921
873 QY TGCAGTGTGAGTGGCTCCACAGCAGAAAACCTATAGGAAAATAATCTTAAATAAATAAAGAA 932
922 Db TGCAGTGTGAGTGGCTCCACAGCAGAAAACCTATAGGAAAATAATCTTAAATAAATAAAGAA 981
933 QY AAAAATCTGAAAAGAAAACAGAGAGGCGAGCTGAGTTATTTGGAGAGCGCTCGCAGGAGAT 992
982 Db AAAAATCTGAAAAGAAAACAGAGAGGCGAGCTGAGTTATTTGGAGAGCGCTCGCAGGAGAT 1041
993 QY AGAAGAAATTTGGAGCGAGAGAGCTGAAAGGAAAATAATAGAGAAAACATCACCTCAGCTGC 1052
1042 Db AGAAGAAATTTGGAGCGAGAGAGCTGAAAGGAAAATAATAGAGAAAACATCACCTCAGCTGC 1101
1053 QY ACCTTCCAAATGACAGGATGCGCAATACCTGCCAGAGGTGAACCTAATAAACAACAGGATT 1112
1102 Db ACCTTCCAAATGACAGGATGCGCAATACCTGCCAGAGGTGAACCTAATAAACAACAGGATT 1161
1113 QY AGAGGAGGCGGCTGAGCGAGAGACTGCAAGAGCAATGCTGAAGCTGAGGACAGGAAGA 1172
1162 Db AGAGGAGGCGGCTGAGCGAGAGACTGCAAGAGCAATGCTGAAGCTGAGGACAGGAAGA 1221
1173 QY GAAAGAGATGCTGAGAAAAGAAAACATTGAAAAGATGAAGATGATGTAGATCAGGAAT 1232
1222 Db GAAAGAGATGCTGAGAAAAGAAAACATTGAAAAGATGAAGATGATGTAGATCAGGAAT 1281
1233 QY TGGACATAGACCTTACCTGATGATAGATCACTTAACCAATGSCCATATTGAGNATGG 1292
1282 Db TGGACATAGACCTTACCTGATGATAGATCACTTAACCAATGSCCATATTGAGNATGG 1341
1293 QY CCATTCTCAGTGGAGCAGCAACTGGACGATGAAGATGATGAAGAGAGCTGCCCCAAA 1352
1342 Db CCATTCTCAGTGGAGCAGCAACTGGACGATGAAGATGATGAAGAGAGCTGCCCCAAA 1401
1353 QY TCTGAGGAATAATCTTTGATGAGCCAAATGCAAGAAAGTGAATACACATATAGCAGCTC 1412
1402 Db TCTGAGGAATAATCTTTGATGAGCCAAATGCAAGAAAGTGAATACACATATAGCAGCTC 1461
1413 QY CTATGAAACAATTCATGTGTGAATTTGCCAAATGACACATAAAATTTCCCGAGTCAAGTT 1472
1462 Db CTATGAAACAATTCATGTGTGAATTTGCCAAATGACACATAAAATTTCCCGAGTCAAGTT 1521
1473 QY CCAGAGTTTTCACCTCGTGTGTTCTCTGATCCTTTAGAACCTGTGGCCTGGCGCTCTGT 1532
1522 Db CCAGAGTTTTCACCTCGTGTGTTCTCTGATCCTTTAGAACCTGTGGCCTGGCGCTCTGT 1581
1533 QY GCTTTCTGAGGATCACCACTTACTGAGCAAGAGGAGAGCAGTCCATCCCATGACAGAG 1592
1582 Db GCTTTCTGAGGATCACCACTTACTGAGCAAGAGGAGAGCAGTCCATCCCATGACAGAG 1641
1593 QY CAGACGGTTTTCAGCTCAGTACTGAGGATTTGCCAAAGCAAAAACCCGGGCGAGCTGA 1652
1642 Db CAGACGGTTTTCAGCTCAGTACTGAGGATTTGCCAAAGCAAAAACCCGGGCGAGCTGA 1701
1653 QY CTGTGTGTGTAATCCCTCGATCCCGGAAATGCGAGTAAATTTAGAGTAAATAATTCCTGA 1712
1702 Db CTGTGTGTGTAATCCCTCGATCCCGGAAATGCGAGTAAATAATTTAGAGTAAATAATTCCTGA 1761
1713 QY CTGTGGAAATGCTTGTGTGGTGCATAAACAATTTACGGAAGACAT-CCAGAGCGGTCACT 1771
1762 Db CTGTGGAAATGCTTGTGTGGTGCATAAACAATTTACGGAAGACATCCCGAGCGGTCACT 1821
1772 QY ACCGCT-CCATAGAGTTTAAATAGAGCGGGGTACAGCACCCCTCGCGACATCTGGAGC 1830

RESULT 10
BC068547
LOCUS

BC068547 2577 bp mRNA linear PRI 06-APR-2004
Homo sapiens SFRS protein kinase 2, mRNA (cDNA clone MGC:87435
IMAGE:5265599), complete cds.

1822 Db ACCGCTCCCATAGAGTTTAAATAGAGCGGGGTACAGCACCCCTCGGACATCTCGAGC 1881
1831 QY ACCGCTGTATGGCATTTTGTAGCTGGCAACCGGAGATTAATTTGTTGAACACCATTTCTGGG 1890
1882 Db ACCGCTGTATGGCATTTTGTAGCTGGCAACCGGAGATTAATTTGTTGAACACCATTTCTGGG 1941
1891 QY GAAGACTATTTCCAGAGACGAAGACACCATAGCCACATCATAGAGTGTCTAGGCAGTATT 1950
1942 Db GAAGACTATTTCCAGAGACGAAGACACCATAGCCACATCATAGAGTGTCTAGGCAGTATT 2001
1951 QY CCAAGGCACTTTGCTCTATCTCGAAAAATTTCTCGGAAATTTCTTCAATCCGAGAGAGAA 2010
2002 Db CCAAGGCACTTTGCTCTATCTCGAAAAATTTCTCGGAAATTTCTTCAATCCGAGAGAGAA 2061
2011 QY CTGCGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTCTGTGAAAAAGTAT 2070
2062 Db CTGCGACACATCACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTCTGTGAAAAAGTAT 2121
2071 QY GGCTGGCCCATGAAGATGCTGCAAGTTTACAGATTTCTCTGATCCCGATGTTAGAAATG 2130
2122 Db GGCTGGCCCATGAAGATGCTGCAAGTTTACAGATTTCTCTGATCCCGATGTTAGAAATG 2181
2131 QY GTTCCAGAAAACGAGCCCTCAGCTGCGAAATGCTTCCGATCCTTGGTTGAATCTTCTAG 2190
2182 Db GTTCCAGAAAACGAGCCCTCAGCTGCGAAATGCTTCCGATCCTTGGTTGAATCTTCTAG 2241
2191 QY CAAATTTACCAATATTGCAATTTCTGAGCTAGCAAAATGTTTCCGATACATTTGGACCTTAAAC 2250
2242 Db CAAATTTACCAATATTGCAATTTCTGAGCTAGCAAAATGTTTCCGATACATTTGGACCTTAAAC 2301
2251 QY GGTGACTCTCATCTTTTAAACAGATTAACAAGTGAAGTGGCTTCATCCTCAGACCTTTTATT 2310
2302 Db GGTGACTCTCATCTTTTAAACAGATTAACAAGTGAAGTGGCTTCATCCTCAGACCTTTTATT 2361
2311 QY TTGCTTTGAGGTTGTTTGAATTTTGTGCACTTTTGTGCACTGTGATCCTGGGGAAGG 2370
2362 Db TTGCTTTGAGGTTGTTTGAATTTTGTGCACTTTTGTGCACTGTGATCCTGGGGAAGG 2421
2371 QY TGATGCTTTT--TGCTTTCAGCTAAAGTAGTTTACTGACCAATTTTCTT-CTGGAAAAAATAA 2427
2422 Db TGATGCTTTTGTGCTCTCAGCTAAAGTAGTTTACTGACCAATTTTCTTCTCTGGAAAAAATAA 2481
2428 QY CAGTCTCTAAGCATTTTCTTGTGTGTGTGAGCAATCAAAATGTCATTTTGTGAAATGA 2487
2482 Db CAGTCTCTAAGCATTTTCTTGTGTGTGTGAGCAATCAAAATGTCATTTTGTGAAATGA 2541
2488 QY AAAATACTTTCCCTTGTGTTTTCGCAAGTGTGTAATTTATGAAGAAATATTTTA 2547
2542 Db AAAATACTTTCCCTTGTGTTTTCGCAAGTGTGTAATTTATGAAGAAATATTTTA 2601
2548 QY GCTGAGTACTATATAATTTTACAAATCTTAAGAAATTTTCAAGTTGGGAAACCAAGAAAAATAG 2607
2602 Db GCTGAGTACTATATAATTTTACAAATCTTAAGAAATTTTCAAGTTGGGAAACCAAGAAAAATAG 2658
2608 QY CAAAGGAAATGACAAATTTTCTTCTGCAAGGAGCATCATTTCTGTATTATAGTGA 2667
2659 Db CAAAGGAAATGACAAATTTTCTTCTGCAAGGAGCATCATTTCTGTATTATAGTGA 2718
2668 QY TGTAAATGCAACCTGTAATTTTGTGATTAATATGAGGAGGGGAGCTCAAAATTTTC 2727
2719 Db TGTAAATGCAACCTGTAATTTTGTGATTAATATGAGGAGGGGAGCTCAAAATTTTC 2777
2728 QY AGAAAAAGCTTAAAAA 2741
2778 Db AGAAAAAGCTTAAAAA 2791

QY 573 CGACATTTCAAGATTTTCAGGCATGAATCGGATACATGTCGATGGTCTTCGAAGTACTTGG 632
DB 631 CGACATTTCAAGATTTTCAGGCATGAATCGGATACATGTCGATGGTCTTCGAAGTACTTGG 690
QY 633 CCACCATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCCAAGTACTTGGT 692
DB 691 CCACCATCTCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCCAAGTACTTGGT 750
QY 693 GAAGAGTATCATTCGACAGCTCTTCAAGGTTAGATTTACTTACACAGTAAGTGCAGAT 752
DB 751 GAAGAGTATCATTCGACAGCTCTTCAAGGTTAGATTTACTTACACAGTAAGTGCAGAT 810
QY 753 CATTCATCTGACATAAAGCCGAAATATCTTGATGTCGTGATGATGATGATGATGATGAT 812
DB 811 CATTCATCTGACATAAAGCCGAAATATCTTGATGTCGTGATGATGATGATGATGATGAT 870
QY 813 AAGAAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCTCTCTCT 872
DB 871 AAGAAATGGCAGCTGAGGCCACTGAGTGGCAGAAAGCAGGTGCTCTCTCTCTCTCTCTCT 930
QY 873 TGCAGTGAATACGGCTCCACAGCAGAAACCTATAGGAAATATCTTAAACCAAAAGAA 932
DB 931 TGCAGTGAATACGGCTCCACAGCAGAAACCTATAGGAAATATCTTAAACCAAAAGAA 990
QY 933 AAAAAGTAAAGAAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 992
DB 991 AAAAAGTAAAGAAACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1050
QY 993 AAGAAATTTGGAGCGAGAGAGCTGAAAGGAAATATAGAGAAACATCACCTCTCAGCTGC 1052
DB 1051 AAGAAATTTGGAGCGAGAGAGCTGAAAGGAAATATAGAGAAACATCACCTCTCAGCTGC 1110
QY 1053 ACTTCCATATGACAGGATGGGAAATCTGCCAGAGGTGAAATCTTAAACCAAAAGAA 1112
DB 1111 ACTTCCATATGACAGGATGGGAAATCTGCCAGAGGTGAAATCTTAAACCAAAAGAA 1170
QY 1113 AGAGGAGGCGCTGAGGAGAGAGCTGCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1172
DB 1171 AGAGGAGGCGCTGAGGAGAGAGCTGCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1230
QY 1173 GAAAGAAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1232
DB 1231 GAAAGAAATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1290
QY 1233 TCGGAAATAGACCTTCACTGAGTGAATCACTTAAACCAATGGCCATATTTAGAGATGG 1292
DB 1291 TCGGAAATAGACCTTCACTGAGTGAATCACTTAAACCAATGGCCATATTTAGAGATGG 1350
QY 1293 CCCATTTCTACTGGAGCAGCACTGACGATGAGATGATGATGAGAGAGCTGCCCAA 1352
DB 1351 CCCATTTCTACTGGAGCAGCACTGACGATGAGATGATGATGAGAGAGCTGCCCAA 1410
QY 1353 TCTGAGGAAATATAATCTTGTAGGAGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1412
DB 1411 TCTGAGGAAATATAATCTTGTAGGAGCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1470
QY 1413 CTATGAACAAATCAATGGTGAATTCGCAATGAGCAGACATAAAATTTCCAGGTCAAGTT 1472
DB 1471 CTATGAACAAATCAATGGTGAATTCGCAATGAGCAGACATAAAATTTCCAGGTCAAGTT 1530
QY 1473 CCCAGAGTTTTCACCTCGTTGTTCTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCTGATCT 1532
DB 1531 CCCAGAGTTTTCACCTCGTTGTTCTCTGATCTTCTGATCTTCTGATCTTCTGATCTTCTGATCT 1590
QY 1533 GCTTTCTGAGGAGTACCACTTACTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1592
DB 1591 GCTTTCTGAGGAGTACCACTTACTGAGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1650
QY 1593 CAGAACGGTTTTCAGCTCTCAGTACTGGGATTTGCCAAAGCAAAACCCGGGAGCTGAG 1652
DB 1651 CAGAACGGTTTTCAGCTCTCAGTACTGGGATTTGCCAAAGCAAAACCCGGGAGCTGAG 1710

QY 1653 CTTGTTGGTGAATCCCCTGGATCCCGGAATCGAGATAAAATTTAGAGTAAAAATTTGCTGA 1712
DB 1711 CTTGTTGGTGAATCCCCTGGATCCCGGAATCGAGATAAAATTTAGAGTAAAAATTTGCTGA 1770
QY 1713 CTTGGGAAATGCTTGTGGTGCATAAACAATTCACGGAAGACATCCAGACGCGTCAGTA 1772
DB 1771 CTTGGGAAACGCTTGTGGTGCATAAACAATTCACGGAAGACATCCAGACGCGTCAGTA 1830
QY 1773 CGGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTCGGACATCTGGAGCAC 1832
DB 1831 CGGCTCCATAGAGTTTAAATAGGAGCGGGTACAGCACCCCTCGGAGCATCTGGAGCAC 1890
QY 1833 GCGCTGTATGGCATTTGAGCTGGCAACGCGGAGATTTATTTGTTGAAACCAATTTCTGGGA 1892
DB 1891 GCGCTGTATGGCATTTGAGCTGGCAACGCGGAGATTTATTTGTTGAAACCAATTTCTGGGA 1950
QY 1893 AGCATTTTCCAGAGACGAAGACCAATAGCCACATCATAGAGTGTCTAGGACGATTTCC 1952
DB 1951 AGCATTTTCCAGAGACGAAGACCAATAGCCACATCATAGAGTGTCTAGGACGATTTCC 2010
QY 1953 AAGGCATTTGCTCTATCTGGAAATATTTCTCGGAAATTTCTTCAATCGCAGAGGAACT 2012
DB 2011 AAGGCATTTGCTCTATCTGGAAATATTTCTCGGAAATTTCTTCAATCGCAGAGGAACT 2070
QY 2013 GGCACACATCAACAAGCTGAAGCCCTGGAGCCCTTTGATGTACTTTGTGAAAAAGTATGG 2072
DB 2071 GGCACACATCAACAAGCTGAAGCCCTGGAGCCCTTTGATGTACTTTGTGAAAAAGTATGG 2130
QY 2073 CTGGCCCATGAAGATGCTGCAAGTTTACAGATTTCTCGATCCCGATCTTGAATTTGTTAGCA 2132
DB 2131 CTGGCCCATGAAGATGCTGCAAGTTTACAGATTTCTCGATCCCGATCTTGAATTTGTTAGCA 2190
QY 2133 TCAGAAAAACGAGCCTGAGCTGGGGAATGCCCTTGGGATCTTGGTGGAAATTTCTTAGCA 2192
DB 2191 TCAGAAAAACGAGCCTGAGCTGGGGAATGCCCTTGGGATCTTGGTGGAAATTTCTTAGCA 2250
QY 2193 AATTTCTACCAATATTTGCAATCTGAGCTAGCAAAATGTTCCAGTACATTCGACCTAAACGG 2252
DB 2251 AATTTCTACCAATATTTGCAATCTGAGCTAGCAAAATGTTCCAGTACATTCGACCTAAACGG 2310
QY 2253 TGACTCTCATTTCTTAAACAGGATTAACAGTGAAGTGTCTGAGCTGGCTTCTCTCAGACCTTTATTTT 2312
DB 2311 TGACTCTCATTTCTTAAACAGGATTAACAGTGAAGTGTCTGAGCTGGCTTCTCTCAGACCTTTATTTT 2370
QY 2313 GCTTTGAGTACTGTTGTTGATCTTCTTTTGTGACATGATCTCTGGGGAAGGTT 2372
DB 2371 GCTTTGAGTACTGTTGTTGATCTTCTTTTGTGACATGATCTCTGGGGAAGGTT 2430
QY 2373 AGTCTTTTGTCTTCAAGTAAAGTGTACTGACCAATTTTCTTCTGGAACAATAACATGT 2432
DB 2431 AGTCTTTTGTCTTCAAGTAAAGTGTACTGACCAATTTTCTTCTGGAACAATAACATGT 2490
QY 2433 CTCTAAGCATTTGTTCTTGTGTTGATGACATTTCAAAATGTCATTTTTTTTGAATGAAAAAT 2492
DB 2491 CTCTAAGCATTTGTTCTTGTGTTGATGACATTTCAAAATGTCATTTTTTTTGAATGAAAAAT 2550
QY 2493 ACTTTCCCTCT 2502
DB 2551 ACTTTCCCTCT 2560

RESULT 11

BC020178
LOCUS
DEFINITION
Mus musculus serine/arginine-rich protein specific kinase 2, mRNA
(cDNA clone MGC:27638 IMAGE:4507346), complete cds.
ACCESSION
BC020178
VERSION
BC020178.1
KEYWORDS
GI:18043213
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

848 TGCACTGAGTACGGCTCCACAGCAAAAACTATAGGAAAAATATCTAAAAACAAGAA 907
933 AAAAAGTGAAGAAAGAAACAGAGGCGAGCTGAGTTATTGGAGAGCGGCTGAGAGAT 992
908 AAAGCTGAAAAAGAAACAGAGGAGACAGGCTGAGTTGCTGGGAAACGCGTACAGGAT 967
993 AGAAGAAATTTGGAGCGAGAGCTGAAAGGAAAAATAATAGAGAAAAACATCACCTCAGCTGC 1052
968 TGAGGAAATTTGGAGCGAGAGCGGAAAGGAAATCTTAGAGGAGAAATCACCTCTGCAGA 1027
1053 ACCTTCC---AATGACCAAGATGGCGAATACCTGCCAGAGGTGAAACTAAAAACACAGG 1109
1028 AGCTTCCGGGAGCAGCAGGATGAGAGTACCAGCGGAGGTGACACTGAAGAGCAGCGA 1087
1110 ATTAGAGGAGGCGGTGAGGCGAGAGACTGCAAAAGGCAATGGTGAAGCTGAGGACAGGA 1169
1088 CTTAGAGGACACAACCTGAGGAAAGAGACAGCAAAAGGATAATGGTGAAGTTGAAGACAGGA 1147
1170 AGAGAAAGAGATGCTGAGAAAGAAAAATTTGAAAAAGATGAAGATGATGATGATCAGGA 1229
1148 AGAGAAAGAGATGCAAGAGAGAGAACCGGGAAGAGGATGAAGATGATGTTGAACAGGA 1207
1230 ACTTGGCAACATAGACCCCTACGTGGATAGAATCACCTAAAAACCAATGGCCATATTGAGAA 1289
1208 ACTTGGCAAACTTAGACCCCTACCTGGGTGGAGTCCCGAAAGCAATGGCCATATTGAA 1267
1290 TGGCCCATTTCTCAGTGGAGCAGCACTGGACAGATGAAGATGATGAAGAGATGAGCGCC 1349
1268 TGGCCCGTTTCTCAGTGGAGCAGCAGCTGGAGGATGAAGAGGAGCATGAAGATGACTGTGC 1327
1350 AAATCTGAGGAATAATACTTGTATGAGCCAAATGCGAAGAGATGATTACACATATAGCAG 1409
1328 AAATCCGAGGAGTAACTCGATGAGCCAAATGCGAGAGTGATTAACGTTATAGCAG 1387
1410 CTCCTATGAACAATCAATGGTGAATTTGCCAAATGAGCAGACATATAAATTTCCCGAGTCACA 1469
1388 CTCCTATGAACAATCAATGGTGAATTTGCCAAATGAGCAACAATAAGACTT----- 1437
1470 GTTCCAGAGTTTTCACCTCGTTGTTCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTG 1529
1438 -----CAGAGTTTCCACACCGTTGTTTCTGGGCGCTTTAGAACCTGTGGCCTGTGGCTC 1492
1530 TGTGCTTCTGAGGAGTACCACTTACTGAGCAAGAGGAGAGCGATCCATCCCATGACAG 1589
1493 TGTGATTTTCCAGAGGAGTCCCACTTACCAGCAGGAGGAGAAAGCGATCCCTCCCATGACAG 1552
1590 AAGCAGAACCGTTTACAGCCTCCAGTACTGGGATTTGCCAAAGCAAAAAACCGGGCAGC 1649
1553 AAGCAGGACAGTTTCCAGCCTCTAGTACTGAGATTTGCCAAAGCAAAAAACCGGGCAGC 1612
1650 TGACTTTGTTGTAATCCCTGATCCCGGGAATGAGATAAAATTTAGAGTAAAAATTCG 1709
1613 TGACCTGTTGGTGAACCTCTGGATCCAGGAATGAGATAAAATTTAGAGTAAAAATTCG 1672
1710 TGACCTGGAATGCTGTTGGTGTGATAAACCTTCCAGGAGAGATCCAGACCGGTCA 1769
1673 TGACCTGGGAATGCTGTTGGTGTGATAAACATTTCCAGAGGATATCCAGACAGGTCA 1732
1770 GTACCCCTCCATAGAGTTTAAATAGGAGGGGTACAGACCCCTCGCGGACATCTGGAG 1829
1733 GTATAGTCCATAGAGTTTAAATAGGAGAGGCTACAGCACCTGAGAGATTTGGAG 1792
1830 CACGGCGTGTATGGCAATTTGAGCTGGCAACCGGAGATTTATTTGTTGAACCAATTCCTGG 1889
1793 TACAGCTTGCATGGCATTTGAGCTCGCCACAGGAGACTATTTGTTGGAACCGCATTCCTGG 1852
1890 GGAAGACTATTCAGAGAGCAAGACCAATAGCCCATCATAGAGCTCTAGGAGAT 1949
1853 GGAAGACTATTCAGAGAGTGAAGACCAATAGCCCATCATAGAGCTCTAGGAGAT 1912
1950 TCCAGGCACTTTGCTCTATCTGAAAAATATTCTCGGGAATTTCTCAATCGAGAGGAGA 2009
1913 CCCAGGCACTTTGCTCTGTTGAAAAATATTCTCGGGAATTTCTCAATCGAGAGGAGA 1972

2010 ACTGGGACACATCAACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGAAAAAGTA 2069
1973 ACTGGGACACATCAACCAAGCTGAAGCCCTGGAGCCTCTTTGATGTACTTGTGAAAAAGTA 2032
2070 TGGCTGGGCCCATGAAGATGCTGCACAGTTTACAGATTTTCTGATCCCGATGTTAGAAAT 2129
2033 TGGCTGGGCCCATGAAGATGCTGCACAAATTTACAGATTTTCTGATCCCAATGTTAGAGAT 2092
2130 GGTTCAGAAAAACGAGCCTCAGCTGGCGAATGCCCTTCGGCATCTCTGTTGGTTGAATTTCTTA 2189
2093 GGTTCAGAAAAACGAGCCTCAGCTGGCGAATGCCCTTCGACATCTCTGGTTGAATTTCTTA 2152
2190 GCAATTTCTACCAATATTGCATTTCTGAGCTAGCAAAATGT- TCCAGTACATTGGACCTAA 2248
2153 GCAGATTTCTACCAATATTAGCATTTCTGAGCTAGCAAAATTTCTCCAGTACATTGGACCTAC 2212
2249 ACGGTGACTCTCATTTCTTAAACAGGATTACAAGTGAAGTGGCTTCTCATCTCTCAGACCTTTA 2308
2213 ACAGTGGCTCTCATTTCTTAAACAGGATTACAGTGAAGTGGCTCCACCTCAGACCTTTG 2272
2309 TTTTCTTTGAGGTACTGTTTGTGACATTTTGTCTTTTGTGCACTGTGATCCTGGGAA 2368
2273 TAGTGTCTTTGAGGTACTGTTTGTGACACTTTTGTCTTCTGTCACCATGCTCCTGGGAA 2332
2369 GGGTAGTCTTTTGTCTTCTGAGCTAAGTAGTTTACTGACCAATTTTCTTCTGGAACAATAAC 2428
2333 GGGTGGTC-TTTTGTCTTCTGAGCTAAGTAGTTTACTGSCCAATTTTCTTCTGGAACAATAAC 2391
2429 ATGTCTCTTAAGCATTTTCTTGTGTTGTGTCACATTTCAAAATGTC-----ATTTTGTGA 2483
2392 ATGTCTCTTAAGCATTTTCTTGTGTTGTGTCACATTTCAAAATGTC-----ATTTTGTGA 2451
2484 ATGAAAAATACCTTCCCTTTGTTTGTGGCAGGTTTGTAACTATTATGAAGAAATAT 2543
2452 ACGAAAAATACCTTCCCTTTGTTTGTGGCAGGTTCTGTAACATTTATTAAGACATAT 2511
2544 TTTAGCTGAGTACTATATAATTTACATCTTAAAGAAATTTATCAAGTTGGGAACCAAGAAA 2603
2512 TTTAGCTGAGTATTATATAATTTACAACTCTTAAGAAATTTATCA--GTTGGAACCAAGAAA 2569
2604 ATAGCAAGGGAATGTACAAATTTTATCTTCGCAAGGAGACATCATCTCTGTTATTATAG 2663
2570 --GAGCAGGAATGTACAAATTTTATCTGTCGCAAGGGAATCAATCTCTGTTATTATAC 2627
2664 T 2664
2628 T 2628

RESULT 12
BC062941

LOCUS BC062941 4287 bp mRNA linear ROD 11-DEC-2003
DEFINITION Mus musculus serine/arginine-rich protein specific kinase 2, mRNA
(cDNA clone IMAGE:6842723), complete cds.

ACCESSION BC062941
VERSION BC062941.1 GI:38566029

KEYWORDS

SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 4287)

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AUTHORS

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McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

GKRFVAMKVISAQHYTTALDEIKLKVRESDPSPDNKDMVQLIDDFKISGNGI
HVMVFYVLGHLLKWIITKSNYQGLPVRVKSIIIRVQLDYLHSSKCKIHTDIKE
NLCMDVYVRWAAEAETKAGAPPSGAVSTAPQKPIGKISNKKKLLKKQ
KROALLKRLQETEEELREAEKRIEENITSAAPSDQDGEYCPVKLKTGTGLEEA
BAETAQNGEAEDQEKEDAKENIEKDEDVDQELANI DPTWIESPKTNHIGNPF
SLEQLDDDEDDCNPENYNDPEPNAESDYTYSSYEQFNGLPNRHKIPEP
PEFSTLSGSLPEPVACGSVLSEGSPLTEQSESSPSHRSRTVSASSTGDLPLKAKTRA
ADLLNPLDPRNADKIRVKIADLGNACWVQKPGQLTCW"

ORIGIN

Query Match		59.9%;	Score 1949.8;	DB 9;	Length 3028;
Best Local Similarity		91.5%;	Pred. No. 0;		
Matches 2168;		Conservative	0;	Mismatches	7; Indels 194; Gaps 2;
QY	153	TCGGAAGAGCGGAGCCTCAACAGAAAGCTCTTTAGTTCCTCTCTCCACCGCCACC	212		
DB	252	TTGCAAGAGCGGAGCCTCAACAGAAAGCTCTTTAGTTCCTCTCTCCACCGCCACC	311		
QY	213	ACCACACACCGCCACCTTTGCCAGACCCACACCCCGGAGCCAGAGGAGATCCT	272		
DB	312	ACCACACACCGCCACCTTTGCCAGACCCACACCCCGGAGCCAGAGGAGATCCT	371		
QY	273	GGGATCAGATGATGAGGAGCAAGAGACCTGCGGACTACTGCAAGAGTGGATATCATCC	332		
DB	372	GGGATCAGATGATGAGGAGCAAGAGACCTGCGGACTACTGCAAGAGTGGATATCATCC	431		
QY	333	AGTGAAATTTGAGACCTCTTCAATGGCGGTATCATGTATTAAGAAAGCTTGGATGGG	392		
DB	432	AGTGAAATTTGAGACCTCTTCAATGGCGGTATCATGTATTAAGAAAGCTTGGATGGG	491		
QY	393	GCACCTTCTACTGTCTGCTGTGGATATGACGGGGAAGATTTGTCGAATGAA	452		
DB	492	GCACCTTCTACTGTCTGCTGTGGATATGACGGGGAAGATTTGTCGAATGAA	551		
QY	453	AGTGTGAAAAGTGGCCAGCATTTATACGGAGACAGCCTTGGATGAAATAAAATTCCTCAA	512		
DB	552	AGTGTGAAAAGTGGCCAGCATTTATACGGAGACAGCCTTGGATGAAATAAAATTCCTCAA	611		
QY	513	ATGTGTTTCGAGAAAGTGATFCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATGAA	572		
DB	612	ATGTGTTTCGAGAAAGTGATFCCAGTGACCCAAACAAAGACATGGTGGTCCAGCTCATGAA	671		
QY	573	CGACTTCAAGATTTGAGGATGAATGGGATACATGTCTGCATGGTCTTGGAGTACTTGG	632		
DB	672	CGACTTCAAGATTTGAGGATGAATGGGATACATGTCTGCATGGTCTTGGAGTACTTGG	731		
QY	633	CCACCATCTCCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCAGTACGTTGTGT	692		
DB	732	CCACCATCTCCTCAAGTGGATCATCAAAATCCAACTATCAAGGCCTCCAGTACGTTGTGT	791		
QY	693	GAAGAGTATCATTCGACAGGTCTTCAAGGGTTAGATTACTTACACAGTAAAGTGAAGAT	752		
DB	792	GAAGAGTATCATTCGACAGGTCTTCAAGGGTTAGATTACTTACACAGTAAAGTGAAGAT	851		
QY	753	CATTCTACTGATCAATAAGCCGGAATAATCTTGATGTGTGGATGATGATATGATGAG	812		
DB	852	CATTCTACTGATCAATAAGCCGGAATAATCTTGATGTGTGGATGATGATATGATGAG	911		
QY	813	AAGAAATGGCAGCTGAGGCGACCTGAGTGGCAGAAAGCAGGTGCTCTCTCTTCCAGGGTC	872		
DB	912	AAGAAATGGCAGCTGAGGCGACCTGAGTGGCAGAAAGCAGGTGCTCTCTCTTCCAGGGTC	971		
QY	873	TGCAGTACTGAGTCCACAGCAAGAACCTTATAGGAAAAATATCTTAAAAACAAAGAA	932		
DB	972	TGCAGTACTGAGTCCACAGCAAGAACCTTATAGGAAAAATATCTTAAAAACAAAGAA	1031		
QY	933	AAAACTGAAAAAGAAACAGAGAGCGGCTGAGTATTTGGAGAGCGGCTCCAGAGAT	992		
DB	1032	AAAACTGAAAAAGAAACAGAGAGCGGCTGAGTATTTGGAGAGCGGCTCCAGAGAT	1091		
QY	993	AGAAAGATTTGGAGCGGAGAGCTGAAAGGAAAAATATAGAGAAAAACATCACCTCCAGCTGC	1052		
DB	1092	AGAAAGATTTGGAGCGGAGAGCTGAAAGGAAAAATATAGAGAAAAACATCACCTCCAGCTGC	1151		

QY	1053	ACCTTCCAAATGACAGAGATGGCGAATACTGCCAGAGAGTGAACTATAAAACACACAGGAT	1112		
DB	1152	ACCTTCCAAATGACAGAGATGGCGAATACTGCCAGAGAGTGAACTATAAAACACACAGGAT	1211		
QY	1113	AGAGAGCGGCTCAGGACAGAGACTGCAAAAGGACAAATGGTGAAGCTGAGGACACAGGAAGA	1172		
DB	1212	AGAGAGCGGCTCAGGACAGAGACTGCAAAAGGACAAATGGTGAAGCTGAGGACACAGGAAGA	1271		
QY	1173	GAAGAAGATGCTGAGAAAGAAAAAATTTGAAAAAGATGAAGATGATGTAGATCAGGAAT	1232		
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QY	1233	TGCGAAACATGACACCTACGTGGATAGAAATCACCTTAAACCAATGCCATATTTGAGATGG	1292		
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DB	1452	TCCTGAGGAATATAATCTTGATGAGCCAAATGCAAGAAAGTGATTTACATATAGCAGTCT	1511		
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DB	1632	GCTTTCTGAGGATCACCACTTACTGACAAAGAGAGAGCAGTCAATCCCATGACAGAAG	1691		
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QY	1633	-----	1632		
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QY	1672	GATCCGCGGAATGCAGATAAAATTTAGAGTAAAAATTTGCTGACCTGGGAAATGCTTGTGG	1731		
DB	1872	GATCCGCGGAATGCAGATAAAATTTAGAGTAAAAATTTGCTGACCTGGGAAATGCTTGTGG	1931		
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DB	1932	GTGCATAAACACTTTCACGGAAGACATCCAGACGGCTCAGTACCGCTCCATAGAGTTTTTA	1991		
QY	1792	ATAGAGCGGGTACAGCACCCCTCGGACATCTTGGAGACAGCGGTGTATGTCATTGAG	1851		
DB	1992	ATAGAGCGGGTACAGCACCCCTCGGACATCTTGGAGACAGCGGTGTATGTCATTGAG	2051		
QY	1852	CTGGCAACGGGAGATTTTGTGTAACCAATTTGGGGAGAGACTATTTCAGAGACGAA	1911		
DB	2052	CTGGCAACGGGAGATTTTGTGTAACCAATTTGGGGAGAGACTATTTCAGAGACGAA	2111		
QY	1912	GACCACATAGCCCATCATATAGAGCTGTAGGAGTATTCCAAGGCACTTTGCTCTATCT	1971		
DB	2112	GACCACATAGCCCATCATATAGAGCTGTAGGAGTATTCCAAGGCACTTTGCTCTATCT	2171		
QY	1972	GGAAAAATTTCTCGGGAATTTCTCAATCGCAG	2003		
DB	2172	GGAAAAATTTCTCGGGAATTTCTCAATCGCAGAGATCATATAGCATTTGATCATTAAGACTG	2231		


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RESULT 14
AB006036
LOCUS AB006036 2300 bp mRNA linear ROD 25-DEC-1997
DEFINITION Mus musculus mRNA for SRPK2, complete cds.
ACCESSION AB006036
VERSION AB006036.1 GI:2723281
KEYWORDS SRPK2.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2300)
AUTHORS Kuroyanagi,N., Onogi,H., Wakabayashi,T. and Hagiwara,M.
TITLE Novel SR-protein-specific kinase, SRPK2,disassembles nuclear
speckles
JOURNAL Biochem. Biophys. Res. Commun. (1998) In press
REFERENCE 2 (bases 1 to 2300)
AUTHORS Hagiwara,M.
TITLE Direct Submision
JOURNAL Submitted (25-JUL-1997) Masatoshi Hagiwara, Tokyo Medical and
Dental University Medical Research Institute, Department of
Endocrinology; Yushima, Bunkyo-ku, Tokyo 113, Japan
(E-mail:m.hagiwara.end@mri.tmd.ac.jp, Tel:03-5803-5836,
Fax:03-5803-5836)
COMMENT Sequence updated (16-DEC-1997).
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polya_site
ORIGIN
Query Match 57.2%; Score 1861.4; DB 10; Length 2300;
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QY 513 ATGTGTTTCGAGAAAGTGTATCCAGTGAGCCCAACAAAGACATGGTGGTCCAGCTATTGA 572
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QY 633 CCACATCTCTCAAGTGGATCATCAAAATCCAAATATCAAGGCCTCCAGTACTGTTGTGT 692
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QY 693 GAAGAGTATCATTCGACAGAGTCTCTCAAGGGTTAGATTACTTACACAGTAAGTCAAGAT 752
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QY	2644	ACATCATTCCTGTATTAGTGTATGTAAATGCACCTGTAAATGTTACTTTGGATT	2703
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Db	2474	ACATCATTCCTGTATTAGTGTATGTAAATGCACCTGTAAATGTTACTTTCCATT	2533
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Search completed: January 23, 2005, 17:20:50
Job time : 13476 secs